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(12) **United States Patent**  
**Beeckman et al.**(10) **Patent No.:** US 9,102,748 B2  
(45) **Date of Patent:** Aug. 11, 2015(54) **GENES INVOLVED IN ASYMMETRIC CELL DIVISION**(75) Inventors: **Tom Beeckman**, Merelbeke (BE); **Ive De Smet**, Ghent (BE); **Steffen Vanneste**, Lauwe (BE)(73) Assignees: **VIB VZW**, Zwijnaarde (BE); **UNIVERSITEIT GENT**, Ghent (BE)

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Aug. 26, 2005 (EP) ..... 05107830

(51) **Int. Cl.****C12N 15/82** (2006.01)**C07K 14/415** (2006.01)**C12N 15/10** (2006.01)(52) **U.S. Cl.**CPC ..... **C07K 14/415** (2013.01); **C12N 15/1003** (2013.01); **C12N 15/1072** (2013.01); **C12N 15/8216** (2013.01)(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to a method to isolate genes involved in the process of asymmetric cell division. The invention relates further to genes isolated using this method, and their use in controlling root formation, preferably lateral root formation.

11 Claims, 7 Drawing Sheets

Figure 1:

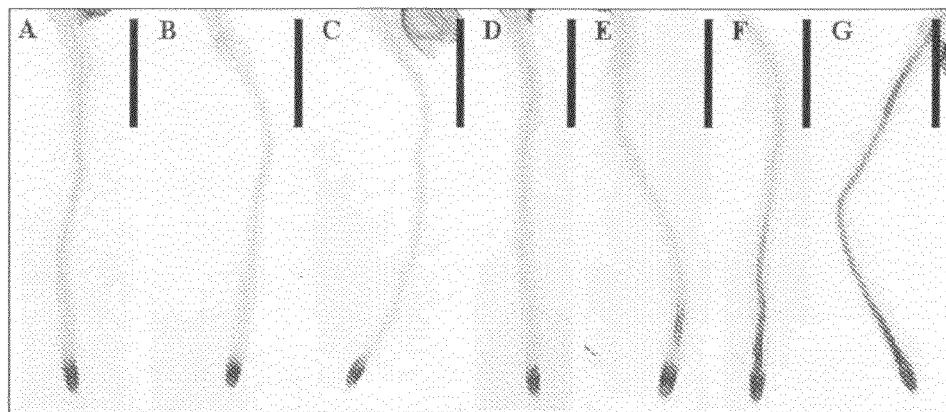


Figure 2:

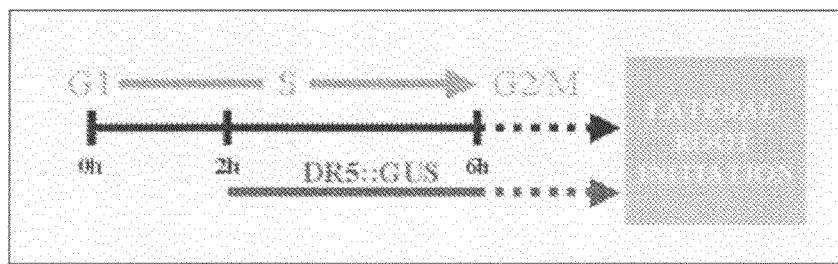


Figure 3:

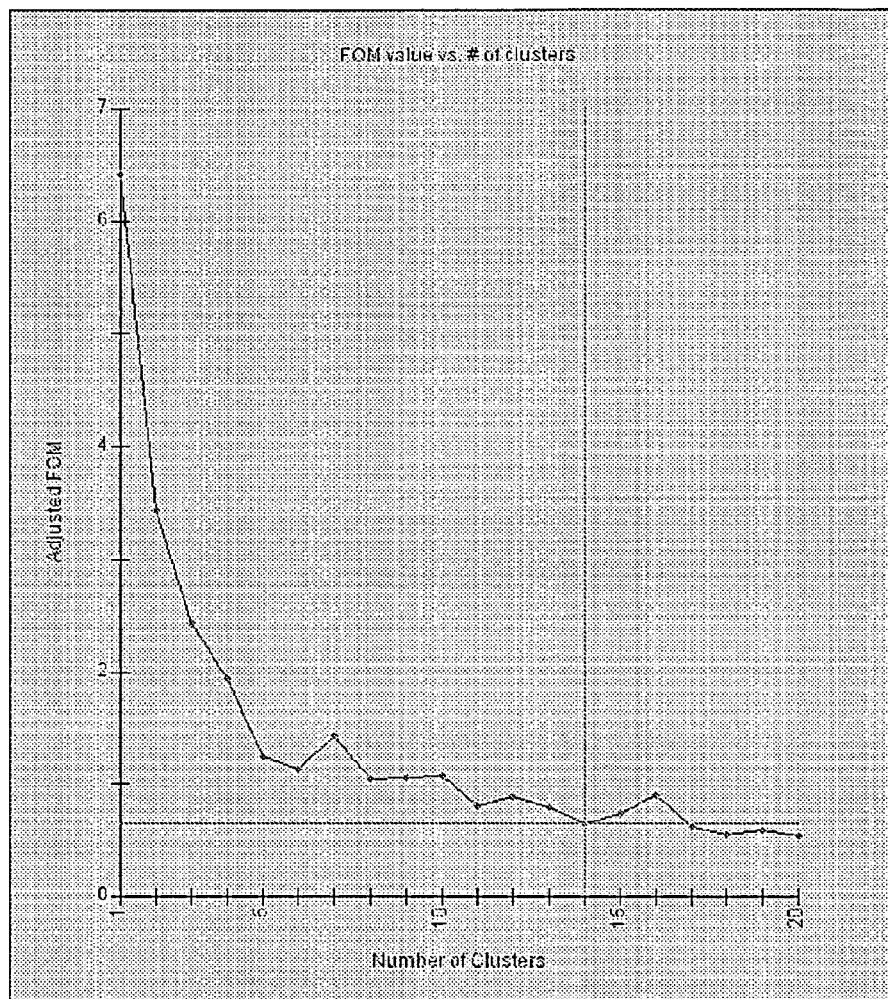


Figure 4:

| solitary root |    |    |    |    |    |    |    |    |     |     |    |    |    |    |
|---------------|----|----|----|----|----|----|----|----|-----|-----|----|----|----|----|
|               | 1  | 2  | 3  | 4  | 5  | 6  | 7  | 8  | 9   | 10  | 11 | 12 | 13 | 14 |
| 1             | 1  | 11 | 10 | 9  | 8  | 7  | 6  | 5  | 4   | 3   | 2  | 1  | 0  | 0  |
| 2             | 2  | 9  | 15 | 2  | 42 | 8  | 12 | 14 | 11  | 9   | 14 | 10 | 12 | 10 |
| 3             | 3  | 4  | 3  | 3  | 21 | 15 | 30 | 14 | 16  | 4   | 20 | 11 | 9  | 7  |
| 4             | 4  | 0  | 2  | 0  | 75 | 24 | 2  | 5  | 48  | 36  | 4  | 16 | 12 | 10 |
| W             | 5  | 0  | 0  | 0  | 6  | 69 | 2  | 0  | 43  | 12  | 0  | 4  | 1  | 0  |
| i             | 6  | 0  | 1  | 2  | 3  | 35 | 16 | 3  | 385 | 51  | 12 | 4  | 1  | 0  |
| d             | 7  | 0  | 5  | 2  | 28 | 4  | 2  | 6  | 6   | 2   | 2  | 2  | 1  | 0  |
| t             | 8  | 0  | 6  | 8  | 15 | 44 | 2  | 13 | 114 | 59  | 9  | 3  | 1  | 0  |
| y             | 9  | 0  | 0  | 1  | 2  | 20 | 2  | 24 | 110 | 195 | 25 | 14 | 4  | 1  |
| p             | 10 | 0  | 0  | 0  | 2  | 21 | 1  | 15 | 63  | 129 | 97 | 32 | 3  | 0  |
| e             | 11 | 0  | 0  | 0  | 2  | 6  | 0  | 8  | 12  | 16  | 29 | 7  | 3  | 4  |
| 12            | 0  | 1  | 0  | 11 | 21 | 0  | 13 | 37 | 160 | 101 | 25 | 28 | 2  | 2  |
| 13            | 0  | 1  | 0  | 2  | 11 | 0  | 10 | 18 | 45  | 88  | 58 | 14 | 11 | 4  |
| 14            | 0  | 1  | 0  | 0  | 3  | 0  | 3  | 3  | 12  | 9   | 9  | 4  | 4  | 7  |

Figure 5:

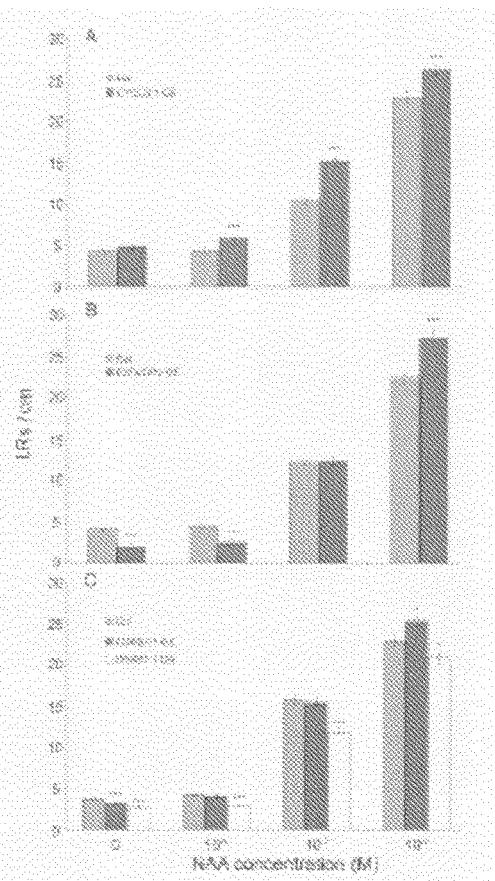


Figure 6:

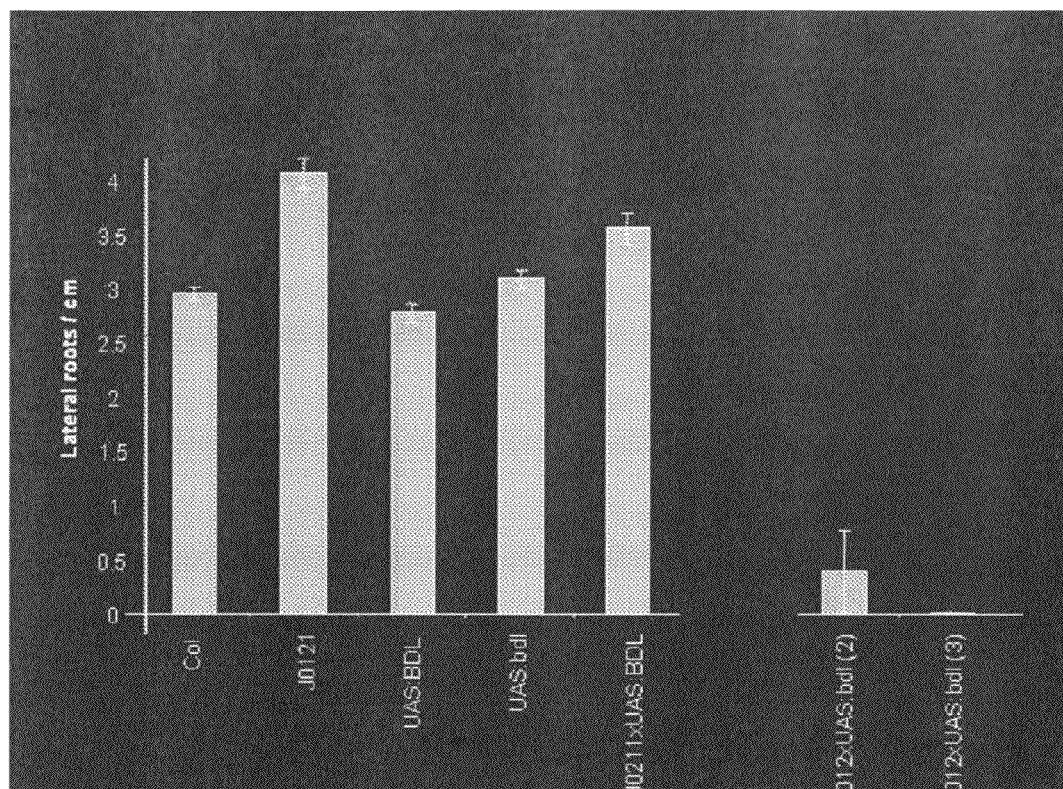


Figure 7:

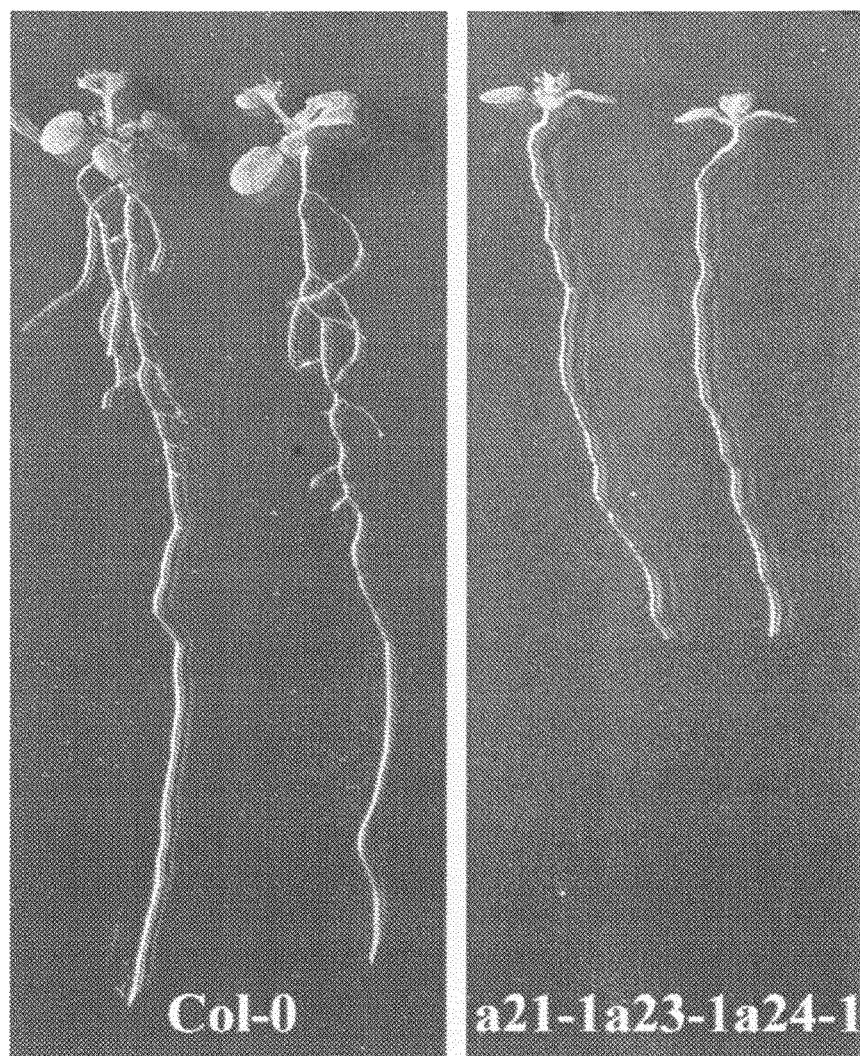


Figure 8:

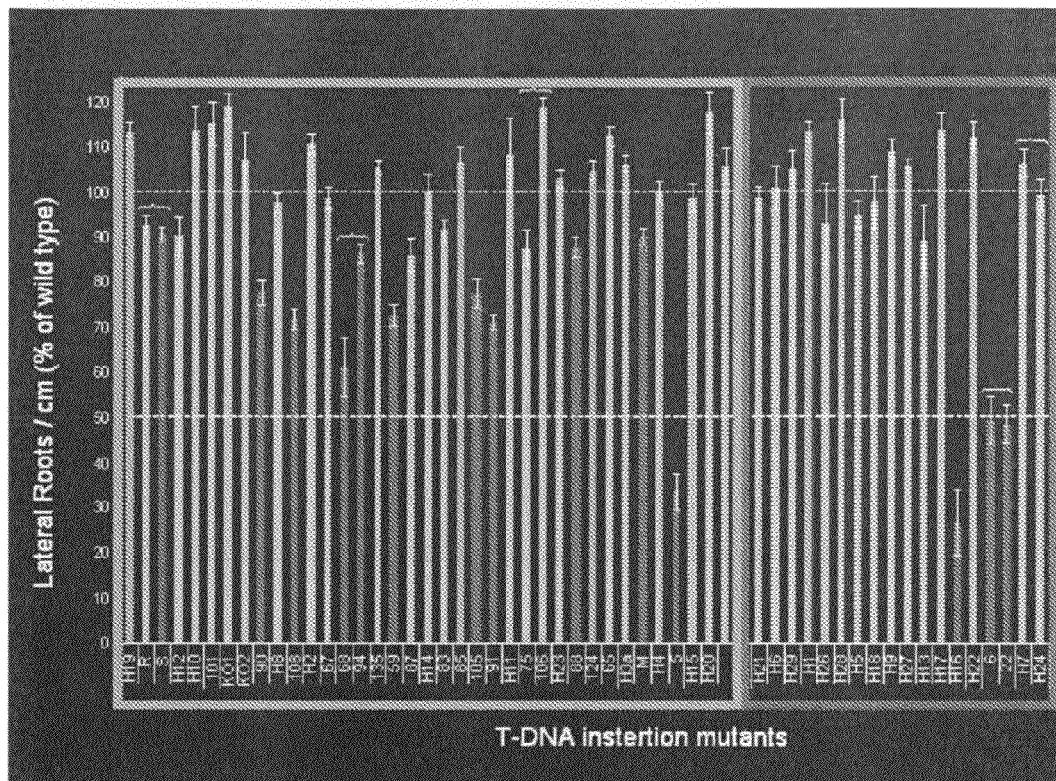
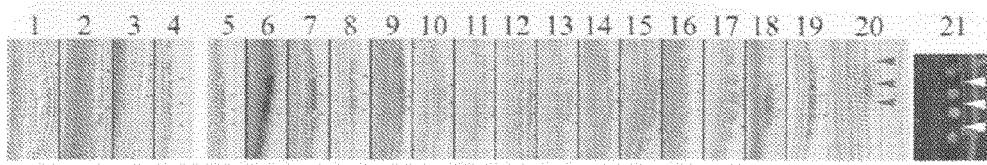


Figure 9:



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## GENES INVOLVED IN ASYMMETRIC CELL DIVISION

### RELATED APPLICATIONS

This application is a national stage application (under 35 U.S.C. 371) of PCT/EP2006/065739 filed Aug. 28, 2006, which claims benefit of European application 05107830.1 filed Aug. 26, 2005.

The present invention relates to a method to isolate genes involved in the process of asymmetric cell division. The invention relates further to genes isolated using this method, and their use in controlling root formation, preferably lateral root formation.

To generate the multitude of different cell types present in multicellular organisms, cell divisions resulting in daughter cells with different fates are vital and decisive in various developmental processes (Scheres & Benfey, 1999). This type of divisions is called asymmetric, whether or not asymmetry is morphologically visible at the time of division (Horvitz & Herskowitz, 1992). Especially in plants, where cell movement is limited, the control of the cell division plane has traditionally been considered important for the formation of regular patterns, i.e. correct divisions during embryogenesis or stomata formation, the formation of ordered cell files in the meristem. (Scheres & Benfey, 1999).

During a plant life cycle, several asymmetric divisions occur: (a) the first division of the zygote (Mansfield & Briarty, 1991); (b) the embryonic division that gives rise to the lens-shaped progenitor cell of the quiescent centre (Dolan et al., 1993); (c) the male microspore division (Twell et al., 1998); (d) divisions during stomatal complex formation (Larkin et al., 1997); (e) oriented periclinal divisions in the early embryo that separate the progenitor cells for the three main tissues, epidermis, ground tissue, and vascular tissue (Jurgens & Mayer, 1994); (f) stem cell divisions that separate differentiation-competent daughter cells and new stem cells in the root (Dolan et al., 1993; van den Berg et al., 1995); and (g) also during lateral root initiation (Casimiro et al., 2003).

Asymmetric divisions fundamentally differ from the standard proliferative divisions in their limited spatio-temporal way of occurrence. Furthermore the number of cells involved is minimal. These characteristics make it difficult to analyze (genome wide) transcript expression during this process.

Up till now only few transcript profiling experiments have been performed, in various organisms, on processes where asymmetric cell divisions are involved, i.e. during gliogenesis in *Drosophila* (Egger et al., 2002), *Arabidopsis* pollen development (Honys & Twell, 2003, 2004; Becker et al., 2003) and lateral root initiation (Himanen et al., 2004). However, none of these approaches aimed at or resulted in the identification of the genetic pathway driving the asymmetric division itself.

In the case of lateral root initiation a few pericycle cells divide anticlinally and asymmetrically (Casero et al., 1993). This is not a continuous process and is exposed to various environmental cues and endogenous signals. Furthermore, these divisions only occur in those pericycle cell files that are in close proximity to the xylem pole (Casimiro et al., 2003).

Micro-array approaches have revealed a broader view on auxin signaling towards LRI (Himanen et al., 2004). For these analyses, a lateral root inducible system was used. In this system, auxin transport, signaling and the G1-to-S cell cycle transition are blocked in seedlings growing on medium supplemented with NPA. Subsequently, these seedlings are transferred to medium containing auxin (NAA) for 1-12

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hours. This allowed an inducible start up of auxin signaling and progression through the G1-to-S transition (Himanen et al., 2002).

An adaptation of this lateral root inducible system can also be used for the study of asymmetric cell divisions. We present a unique approach that allowed us to circumvent problems like tissue specificity and the limited number of cells involved through isolating specifically asymmetrically dividing pericycle cells at the xylem pole during LRI. Therefore we combined 4 strategies: 1) a recently developed lateral root inducible system, that synchronously induces the asymmetric divisions during LRI (Himanen et al., 2002), 2) a xylem pole pericycle specific GFP marker line (J0121), 3) a Fluorescent Assisted Cell Sorting approach (Birnbaum et al., 2003), and 15 4) genome-wide micro array analysis on the isolated xylem pole pericycle cells. This combined strategy allowed us not only to identify those genes involved directly in the LRI process but also to extrapolate the results to the general concept of asymmetric division. We found, as potential regulators 20 of asymmetric divisions, genes involved in cell cycle regulation and a high percentage of genes associated with cytoskeleton organization and dynamics.

It is a first aspect of the invention to provide a method to isolate genes involved in asymmetric cell division, comprising: 25 (1) subjecting roots of a wild type plant to a treatment inducing lateral root initiation in a synchronous way; (2) subjecting roots of a mutant not developing lateral roots by a defect in auxin signalling to a treatment inducing lateral root initiation in wild type in a synchronous way; (3) identifying 30 genes that are induced in wild type but not in mutant; (4) identifying genes induced in the xylem pole pericycle in wild type during lateral root initiation. Early lateral root initiation as used here means the events at different stages just prior to the first division in the pericycle. Preferably this is within 10 hours after auxin induction of the lateral root, more preferably within 8 hours of said induction, even more preferably 6 hours after said induction. Preferably, the mutant used is a slr-1 mutant.

Preferably, said method is further comprising the use of a 40 xylem pole pericycle marker line, followed by cell sorting. Even more preferably, said marker is GFP. Most preferably, the isolated cells are genome wide analysed by microarray analysis

Another aspect of the invention is a gene involved in early 45 lateral root formation, isolated with the method according to the invention. Preferably, said gene encodes a transcription factor. Even more preferably, said transcription factor is selected from the group consisting of SEQ ID No 1 to SEQ ID No 19.

As transcription factors often are expressed in the tissue of 50 activity, their promoters are likely to be of economical use. Such promoters can be used in several strategies to enhance pathogen tolerance/resistance of the plant.

Another aspect of the invention is a gene involved in asymmetric cell division, isolated with the method according to the 55 invention. Preferably said method is the method further comprising the use of a xylem pole pericycle marker line, followed by cell sorting. Even more preferably, said gene is comprising a sequence encoding a protein selected from the group consisting of SEQ ID No 20-SEQ ID No 34, or a homologue thereof.

Still another aspect of the invention is a transcription factor 60 involved in early lateral root formation, whereby said transcription factor is selected from the group consisting of SEQ ID No 1 to SEQ ID No 19. Preferably, the gene encoding said transcription factor is isolated with the method of to the invention.

A further aspect of the invention is the use of a gene, isolated with the method of the invention, to modulate early lateral root initiation. Modulation as used here may be an increase or a decrease in number of lateral roots, it may be an increase or decrease in size of the lateral roots or it may be a shift in time (earlier or later in plant development) of lateral root formation. Preferably, said modulation is an increase or decrease in lateral roots, even more preferably it is an increase in lateral roots. Preferably, said gene is encoding a transcription factor. Even more preferably, said gene is encoding a transcription factor selected from the group consisting of SEQ ID No 1 to SEQ ID No 34, or a homologue thereof. Said genes may be used in combination to increase the effect on lateral root formation

Gene as used here refers both to the genomic sequence (including possible introns) as well as to the cDNA derived from the spliced messenger. It may refer to the promoter sequence too. However, it is clear for the person skilled in the art that for some applications, the coding sequence, such as it may be derived from the cDNA, may be operably linked to a suitable promoter. Operably linked refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A promoter sequence “operably linked” to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the promoter sequence.

A homologue as used here means that the protein encoded by the gene has an amino acid sequence that is at least 75% identical, and even more preferably at least 80% identical, and even more preferably at least 85% identical, and even more preferably at least 90% identical and even more preferably at least 95% identical, and even more preferably at least 96% identical, and even more preferably at least 97% identical, and even more preferably at least 98% identical, and even more preferably at least 99% identical, as measured by a BLASTP search (Altschul et al., 1997)

#### BRIEF DESCRIPTION OF THE FIGURES

FIG. 1: Lateral root inducible system (A-G) Time-series of 12 h of NM treatment (blue staining=P::GUS reporter activity of Arath;CYCB1;1 marking G2/M transition) The auxin transport inhibition blocks all lateral root initiation, allowing synchronous induction of lateral roots via auxin, resulting in the onset of G2/M transition 6 to 8 h after transfer to auxin medium (D,E)

FIG. 2: Scheme of main events during lateral root initiation

FIG. 3: Figure Of Merit calculation for a range to 20 clusters

FIG. 4: Cross-table representation with the frequencies of all combinations of expression profiles

FIG. 5: Overexpression phenotype of CYCD3;1, E2Fa/DPa and CDKB1;1 in 10 day old seedlings, as compared to wild type

FIG. 6: Xylem pole pericycle specific expression of a stabilised mutant version of the BDL protein in J0121xUAS:bd1 ( $0.0 \pm 0.0$ ), resulting in a lateral rootless phenotype, while the control lines Col-0 ( $3.0 \pm 0.1$ ), J0121 ( $4.1 \pm 0.1$ ), UAS:bd1 ( $3.1 \pm 0.1$ ), UAS:BDL ( $2.8 \pm 0.1$ ) and J0121xUAS:BDL ( $3.6 \pm 0.1$ ) display no reduction in the number of lateral roots/cm

FIG. 7: Combined mutations in various members of the CYCA2;4 family results in dramatic reductions of lateral root density (left panel: Col-0 control; right panel: multiple mutant)

FIG. 8: Analysis of the lateral root phenotype of several homozygous SALK T-DNA insertion mutants, derived from genes in various clusters. The code of the mutants is listed in Table 5.

FIG. 9: Detailed analysis during early lateral root formation (asymmetric cell division is indicated by arrowheads) of various up and down regulated genes in the complete dataset. The numbers refer to the fusions listed in Table 6.

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#### EXAMPLES

##### Materials & Methods to the Examples

###### WT Col—Slr Comparison Based Approach

###### Sampling

In the lateral root inducible system seeds (Col-0 & slr-1) were germinated on standard Murashige & Skoog media containing 10  $\mu$ M N-NaphthylPhthalamic Acid (NPA) on vertically oriented square plates (Greiner Labortechnik, Frickenhausen, Germany) in a growth chamber under continuous light (110  $\mu$ E·m<sup>-2</sup>·s<sup>-1</sup> PAR supplied by cool-white fluorescent tungsten tubes [Osram, München, Germany]) at 22° C. (Himanen et al., 2002). 72 h after germination (0 h time-point), only those seedlings (wild-type & mutant) that made full contact with the medium were transferred to medium containing 10  $\mu$ M NaphthylAcetic Acid (NAA) and harvested after 2 h and 6 h. These 3 time-points were applied for both wild-type and mutant. A mock treatment was included for wild-type only, by transferring the seedlings to standard Murashige & Skoog medium without NAA addition. For all time-points only the lateral root inducible segments were used for the analysis. For this purpose the root apical meristem and hypocotyl were manually removed to minimise contamination with other cell types. All treatments were repeated.

###### Microarray and Clustering

RNA was extracted using the RNeasy Minikit (Qiagen). RNA quality and quantity were analysed using RNA 6000 Nano Lab Chip Kit (Agilent Technologies, Germany). For microarray 5.8  $\mu$ g total RNA was used. Double stranded cDNA was synthesized with Life Technologies cDNA Synthesis Kit. The double stranded cDNA was converted to biotin-labelled cRNA (Ambion MEGA script T7 in vitro transcription kit and biotin containing ribonucleotides from Enzo (LOXO GmbH)). 15  $\mu$ g of fragmented cRNA was used for hybridization to ATH1 Affymetrix® gene-chips. The biotin-labelled RNA was visualised with phycoerythrin-streptavidin labels. ATH1 gene-chips (Affymetrix) represent 22747 *Arabidopsis* genes (~85% predicted genes in the *Arabidopsis* genome).

The overall signal of the different chips was normalized using Microarray Suite 5.0 software (Affymetrix). The raw data were exponentially distributed and were therefore  $\log_2$ -transformed before further statistics. Statistical significance was analysed via ANalysis Of VAriance (ANOVA) for every gene. This resulted in a p-value for three sources of variance: the effect of the time-course, the effect of the genotype and the effect of their interaction. For the genome-wide transcript profiling the stringency was increased to  $p < 0.001$ . This is the equivalent of 23 false positive tests if 22747 tests are performed. At this level of significance 3110 genes were flagged.

As we need to detect differences between the expression profiles in both genotypes we needed a tool to optimally visualise these differences. We obtained this tool by merging time-course data for both genotypes per time-point. This merged dataset was subsequently treated as if it was a single time-course (repeated time-points are indicated with \*) (0/0\*/2/2\*/6/6\*). Before clustering, an estimate of the predictive

power of a clustering algorithm (Figure Of Merit) was computed over a range of clusters. The lower the Figure Of Merit, the higher the predictive power of the clustering will be (Yeung et al., 2001). The number of clusters, for which the smallest increment did not result in a decrease of the Figure Of Merit, was chosen as the optimal cluster number. All clustering computation was performed using TIGR Multi-experiment Viewer 2.2 (tigr.org webpage, Oct. 11, 2003).

Each gene was related to two clusters, representing its average expression profile in both wild-type and mutant. The combinational potential was represented in a cross-table format with indication of the frequency of occurrence of each combination. As an indicator of differences between clusters, a colour code was applied. For all clusters, the relative induction/reduction rates of the expression profiles between 0 h and 2 h and between 0 h and 6 h of the average profiles were compared to one another. If these relative induction/reduction rates differed 2-fold or more at one of these levels of comparison an orange or blue colour was assigned to this cluster combination. If these relative induction/reduction rates differed at both levels 2-fold or more, a red colour was assigned to this cluster combination. A cluster was considered as up-regulated when the rate of induction of the expression level was stronger than 2-fold for both intervals (0-2 and 0-6). Only clusters 1, 2, 3 and 4 met these criteria.

#### Cell Sorting Approach

##### Sampling

In the lateral root inducible system seeds (J0121, plantsci.cam.ac.uk/Haseloff/geneControl/catalogues/Jlines/record/record\_0.html webpage) were germinated (Himanen et al., 2002). As described above, seedlings were harvested after 2 h and 6 h. For all time points the roots were cut into small 0.5 mm fragments, and those segments were protoplasted according to Birnbaum et al. (2003, 2005). GFP expressing cells were isolated on a fluorescence activated cell sorter (Becton Dickinson FACS Vantage). The cells were sorted directly into lysis buffer (Qiagen RLT buffer), mixed and immediately frozen at -80° C. for later RNA extraction. All treatments were repeated.

##### Microarray and Clustering

Standard Affymetrix protocols for small samples were then used for amplifying, labeling and hybridizing RNA samples (wi.mit.edu/CMT/protocols/AffySmlSamplProto.pdf webpage). Then hybridized cRNA was fragmented as described in the GeneChip® Expression Analysis Technical Manual. The hybridization, washing and staining steps were performed according to the Affymetrix protocols (wi.mit.edu/CMT/protocols/Affymetrix%20User%20Manual.pdf webpage).

The data were processed using a Mixed Model. This mixed-model analysis of variance was performed to identify genes differentially expressed between the various treatments (Chu et al., 2002, 2004). In this approach, a global normalization step was applied to minimize general array-level effects by centering the mean of the  $\log_2$ -transformed values to zero for each array (Chu et al., 2002). Outlier probes with values greater than two standard deviations from the probe-set mean were then removed. Next, a mixed-model ANOVA was applied to the transformed and centered intensity values obtained from the global normalization step. This gene model, which is based on that developed by Chu et al. (2002), can be formalized as:

$$\log_2(PM_{jkl}) = T_j + P_k + A_{l(j)} + \epsilon_{jkl}$$

where the PM variable refers to the output of the global normalization procedure for each gene, as described above. The symbols T, P, and A represent treatment, probe, and array

effects, respectively. The array effect  $A_{l(j)}$  is assumed to be a normally distributed random effect (Chu et al., 2002). A standard error term  $\epsilon_{jkl}$  was also applied to this model. In addition, the indices j, k, and l represent the jth treatment, on the kth probe, and on the lth replicate (Chu et al., 2002). The output of this model is the mean expression value for every gene, based on the global model, as well as a p-value from the gene-model for the probability of falsely rejecting the null hypothesis of no-differential expression ( $\alpha=0.05$ ). The global and gene models were run on a Linux server with the statistical software SAS (version 8.2).

Grouping of the 1920 significantly differentially expressed genes coming out of the statistical analysis into 10 clusters, was done using TIGR MeV 3.0.3 (Saeed et al., 2003).

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#### Example 1

##### Sampling and Microarray Analysis

Recently, we developed an auxin-based lateral root inducible system (Himanen et al., 2002). Based on this unique, in planta inducible system we performed a genome-wide transcript profiling, to identify key regulators of lateral root initiation. To facilitate the identification of those genes with a role in auxin signalling in relation to lateral root initiation a mutant was included as a negative control. The mutant (solitary root) was mainly selected for its inability to form lateral roots and because the affected gene is involved in a known part of auxin signalling (Fukaki et al., 2002). The comparison of wild-type and mutant in the lateral root inducible system is of fundamental importance to select genes involved in lateral root initiation, downstream of the protein affected in the mutant (IAA14/SLR).

Time-points were chosen in such a way that we could monitor gene expression at different stages just prior to the first division in the pericycle. Himanen et al. (2002) showed that this event occurs 8 to 10 h after transfer to auxin containing medium. The zero time-point (72 h NPA) is consistent with a G1/S-blocked state, while 6 h after transfer to auxin 35 pericycle cells adjacent to the xylem poles are nearly starting G2/M transition. Furthermore, the earliest auxin response in the root was visualised with a DR5::GUS reporter 1.5 to 2 h after auxin treatment (FIG. 2). Therefore, a time-point (2 h NAA) was included to represent this earliest auxin-modulated transcription.

Both wild-type and mutant (slr-1) were subjected to these treatments. Additionally, a mock-treatment was included for wild type to assess differential gene expression due to the transfer. All treatments were biologically repeated adding to the statistical significance of the data.

#### Example 2

##### Statistical Analysis and Clustering

After normalisation and transformation, the data were subjected to ANOVA analysis. Comparison of the previous limited transcript profiling (on 4600 genes) (Himanen et al., unpublished results) with the present one, clearly shows that our lateral root inducible system is highly reproducible, since 64% of the differentially expressed genes were confirmed when checked at the same level of significance ( $p<0.005$ ). In order to reduce the amount of false positives even further, we applied a 5-fold higher stringency ( $p<0.001$ ) than in the previous transcript profiling. At this high stringency level still 3110 genes were differentially regulated. Clustering of all data-points for both wild-type and solitary root separately did

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not meet our needs to assess the differences in expression profiles in both genotypes. In order to meet this criterion, the data for both genotypes were combined in one dataset. Each gene was represented twice in the combined dataset, resulting in 6220 expression profiles. In order to estimate the optimal number of clusters, the Figure Of Merit (FOM) was computed for a range of clusters. The smallest FOM was estimated at 14 clusters, representing the optimal number of clusters corresponding to the highest predictive power (FIG. 3).

Subsequently, all 6220 expression profiles were clustered into 14 clusters. In this way two coordinates were assigned per gene, representing the expression profiles in both genotypes. All 196 (14×14) potential combinations are represented in FIG. 4 together with the absolute frequency of genes in each combination. Differences between clusters are indicated through a colour code.

The genes indicated in red (305) represent the genes for which wild-type gene expression is always higher than in solitary root. Genes of this kind, induced in wild-type and less in solitary root, are most likely involved in lateral root initiation. Therefore we focused on the genes, represented as cluster 1, 2, 3 and 4 in wild-type. In this way we could narrow down the total number of significantly regulated genes (3110) to 266 (~9%) that might have a crucial role in lateral root initiation.

#### Example 3

##### Effect of Filtering on General Functional Categories

A comparison of the percentages of genes belonging to a functional category before and after clustering according to MATDB (MIPS *Arabidopsis Thaliana* DataBase) nicely illustrates the effectiveness of our cross-table based clustering (Table 1). The filtering procedure clearly resulted in an enrichment for genes related to cell cycle, RNA processing, DNA synthesis and signalling and development. These features confirm that the monitoring of cell cycle progression in the pericycle is possible using our lateral root inducible system. Furthermore, we found a higher percentage of genes involved in transcriptional regulation, indicating that there is a general need for increased transcriptional activity. The percentage of unclassified and unknown genes remains about at the same level. Moreover, a strong relative reduction of genes involved in stress, transport and metabolism was achieved through the applied selection criteria. Besides, the drop in the number of genes involved in transport might also be categorised as a drop in number of genes related to detoxification and stress responses.

#### Example 4

##### Cell Cycle Regulation During Lateral Root Initiation

Detailed examination of the selection reveals G1/S and S-phase markers such as Arath;CYCD3;2 and Arath;CYCA2;4. Furthermore, the link to S-phase entry/progression is never far-off as there is a high representation of genes involved in DNA replication and protein synthesis. This underlines the suitability of our approach to study auxin mediated cell cycle regulation. As interesting as core cell cycle events can be, they require upstream signalling cascades such as auxin signalling.

#### Example 5

##### Auxin Signalling During Lateral Root Initiation

In our stringent selection, several genes were detected belonging to gene families with known roles in auxin signal-

ling such as Aux/IAAs, ARFs, ATGH3s and an ATSAUR (Hagen & Guilfoyle, 2000). Different mutants in genes belonging to the Aux/IAA gene-family have lateral root phenotypes (Fukaki et al., 2002; Park et al., 2002). Their gene-products act to repress the activity of ARF transcription factor dimers (Leyser, 2002).

Recently, researchers gained insight into the function of ATGH3-gene products, through the analysis of activation tagged lines (Takase et al., 2004). Several of these GH3 proteins have been shown to adenylate plant hormones and based on their substrate specificity and protein structure, they are subdivided into three major classes (Staswick et al., 2002). The members of group II, such as ATGH3-1, ATGH3-5 and ATGH3-6/DFL1, can adenylate IAA, negatively regulating auxin activity (Takase et al., 2004).

As for the Small Auxin Up RNAs (ATSAUR), very little is known about their function in auxin response. However, their auxin inducibility has been reported for several years (McClure & Guilfoyle, 1989).

#### Example 6

##### New Genes in Lateral Root Initiation: Transcription Factors

As transcription factors play central roles in patterning and development (Sabatini et al., 2003), it is obvious that such genes in our selection (19) will be of particular importance in the signalling cascades during lateral root initiation (Table 1). Most of the genes of this selection were recently shown to be specifically expressed in stele tissue (including the pericycle) by a transcript profiling study of the *Arabidopsis* root tip (Birnbaum et al., 2003), justifying the selection criteria used in our study.

Interestingly, two of the AP2 domain transcription factors belong to the same subclade. This implicates that it is likely that these genes have redundant functions. Furthermore, there is one AP2 domain transcription factor that belongs to this same subclade of three genes, which is not represented on the microarray (Alonso et al., 2003). We hypothesize that this gene (At4g27950) could also be functionally redundant to the two other members of this subclade. Consequently, this gene was also added to our selection, bringing the final number of our selection to 20 genes.

Within our dataset there are 15 transcription factors for which no role in auxin signalling has been suggested. As for a start of validation it will be of our primary interest to do a functional analysis on these transcription factors with respect to lateral root initiation.

Many of these transcription factors have great potential for involvement in lateral root development, as they have homologues for which a role in organ development has been reported. The ABI3-gene was previously described as a seed-specific gene, but recently it has been shown to have a role in auxin signalling and lateral root development (Brady et al., 2003). Also, AP2 and several homeobox genes have been shown to be involved in floral organ development, which implies that homologs have great potential to be essential in the development of other organs such as lateral roots (Carpenter & Coen, 1990; Maes et al., 1999).

Interestingly, there is one transcription factor, MYB124, for which the mutant has an aberrant stomatal development. As the result of the mutation stomata with four guard cells are formed instead of two (Yang & Sack, 1995). Its upregulation upon auxin treatment of the root implicates that the MYB124

gene-product might have an as crucial role in the formative divisions in the pericycle (lateral root initiation) as it has in stomatal development.

#### Example 7

##### Identifying Asymmetric Cell Division Genes

Using LRI as a model to genetically dissect the asymmetric cell division, we investigated within our 10 clusters, which cluster contained the putative regulators of this type of division. First, we analyzed which cluster is strongly linked with the G2-to-M transition by verifying the expression profile during cell cycle progression using the genome wide expression data for synchronized *Arabidopsis* cell suspensions (Menges et al., 2003). We found that 48% of the genes in cluster 3 peaked at the G2-to-M transition. This is opposed to less than 10% of the genes that peaked at this transition in all the other clusters. This is a strong overrepresentation of G2-to-M related genes within this cluster as compared to the other clusters. Furthermore, this is 59% of the G2-to-M specific genes present in the whole dataset.

Secondly, we analyzed which cluster is potentially correlated with asymmetric cell division. For this we used protein sequences of genes that are assigned to the functional categories ([godatabase.org/cqi-bin/amigo/go.cgi](http://godatabase.org/cqi-bin/amigo/go.cgi)) “asymmetric cell division” and/or “establishment and/or maintenance of cell polarity” in a wide variety of organisms (i.e. *Caenorhabditis elegans*, *Drosophila melanogaster*, *Schizosaccharomyces pombe*, mouse . . . ). We performed a protein blast analysis with the protein sequences of various organisms and those *Arabidopsis* protein sequences of the genes assigned to our different clusters. This resulted in an overrepresentation of 54 genes putatively correlated with “asymmetric cell division”, “cell fate commitment” and/or “establishment and/or maintenance of cell polarity” in cluster 3.

To further analyze the process of asymmetric cell division, we therefore focused on the 340 genes within cluster 3. Within this cluster, 25% of the genes have been described; the remaining 75% is unknown, expressed, hypothetical or putative.

In order to even further reduce the number of interesting candidates; we subtracted those genes of which involvement in normal cell division (synchronized, dividing *Arabidopsis* cell suspension cells) is shown (Menges et al., 2003). After that analysis we ended up with 190 candidates potentially involved in asymmetric cell division.

#### Example 8

##### Meta-Analysis for Improvement of the Results

It has been previously demonstrated that cell cycle progression in the pericycle is not sufficient for SOLITARY ROOT/IAA14-mediated lateral root initiation in *Arabidopsis thaliana* (Vanneste et al., 2005).

To support this finding we analyzed the root phenotype of transgenic lines over-expressing (35S) cell cycle genes. Based on the cell cycle stage specific expression profiles upon lateral root induction shown in Himanen et al. (2002) and our dataset, we selected CYCD3;1 (G1-to-S and G2-to-M, Dewitte and Murray, 2003), E2Fa/DPa (G1-to-S, De Veylder et al., 2002) and CDKB1;1 (G2-to-M, Boudolf et al., 2004). The over-expression phenotype in 10 day old seedlings of all lines was analysed and compared to WT (FIG. 5). None of the transgenic lines showed a significant increase in the lateral root density. The double transgenic over-expression line of

E2Fa/DPa even showed a strong decrease in the lateral root number compared to the wild type Col. Also over-expression of CDKB1;1 resulted in fewer lateral roots. Furthermore, in the case of CDKB1;1, the over-expression of dominant negative allele of CDKB1;1 (CDKB1;1.N161) (Boudolf et al., 2004), resulted in a stronger decrease of the number of lateral roots.

Next, we analyzed if auxin (NAA) application in combination with increased cell cycle gene expression could result in a higher number of lateral roots compared to the auxin or cell cycle alone. We therefore transferred 5 day old seedlings of the above mentioned transgenic *Arabidopsis* lines of E2Fa<sup>OE</sup>, DPa<sup>OE</sup>, CYCD3;1<sup>OE</sup> and CDKB1;1<sup>OE</sup> to increasing concentrations of auxin ( $10^{-8}$ ,  $10^{-7}$  and  $10^{-6}$  M of NAA) and analysed, after another 5 days of growth, their ability to initiate lateral roots. We found a significant increase in the CYCD3;1<sup>OE</sup> opposed to the wild type. Similarly, the number of LRs/cm could be significantly increased in the E2Fa/DPa<sup>OE</sup> transgenic line, until exceeding the wild type number at high auxin concentration. Even CDKB1;1<sup>OE</sup> exceeded the WT number upon auxin application, while this was not the case for the CDKB1;1 DN<sup>OE</sup> line.

The above results indicate that stimulating the basic cell cycle machinery is not sufficient for de novo lateral root initiation but when extra auxin is provided the enhanced cell cycle competence can be exploited to produce new organs. This corroborates the suggestion by Vanneste et al. (2005) that, next to cell cycle activation, another factor is required to specifically drive lateral root initiation.

Notwithstanding a putative function for CDKB1;1 in lateral root initiation, cell cycle genes are clearly not the key regulators for lateral root initiation. Hence, we searched within our dataset for potential specific regulators of lateral root initiation via meta-analysis. This meta-analysis was performed to reduce the number of genes from 1920 significant genes to 15 highly interesting candidates (Table 3). The analysis involved subsequent steps of overlapping and in depth analysis of subsets of genes as described below.

- 1) Affymetrix *Arabidopsis* ATH-1 Genome Array (22758 genes);
- 2) Unique significantly differentially expressed genes (1920);
- 3) Upregulated genes in asymmetric cell division during lateral root initiation after selecting 1 cluster based on the following criteria (340) using in depth analysis with functional categories terms:  
highest % G2-M genes  
highest % genes involved in asymmetry  
highest % genes involved in polarity  
highest % genes involved in cell fate;
- 4) Genes potentially involved in cell fate and cell polarity (190) after subtracting the mitotic apparatus based on Menges et al. (2003);
- 5) Genes involved in auxin-induced cell fate and/or cell polarity in the xylem pole pericycle during lateral root initiation (15) after overlapping the remaining 190 genes with those lateral root initiation genes (913) depending on rapid SLR/IAA14 degradation for normal auxin responsiveness, as derived from the cross table (FIG. 4).

#### Example 9

##### BDL is Involved in Lateral Root Initiation

As was determined earlier (Vanneste et al., 2005), an important regulator mechanism for lateral root initiation is auxin signaling and transport. Table 4 lists the genes involved in those events and demonstrates that most of them are early

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up/down regulated. A number of genes have been shown to be involved in lateral root formation (ALF1/RTY/SUR1, Celenna et al., 1995, King et al., 1995, Boerjan et al., 1995; DFL1, Nakazawa et al., 2001) and for several Aux/IAAs and ARFs a role in lateral root initiation and/or formation was shown earlier (IAA19/MSG2, Tatematsu et al., 2004; ARF19, Wilmoth et al., 2004; IAA1/AXR5, Yang et al., 2004; IAA3/SHY2, Tian and Reed, 1999).

For BDL/IAA12, part of a pair of transcriptional regulators with MP/ARF5, we demonstrate the involvement in lateral root initiation. Xylem pole pericycle specific expression of a stabilised mutant version of the BDL protein in J0121xUAS: bdl ( $0.0\pm0.0$ ) resulted in a lateral rootless phenotype, while the control lines Col-0 ( $3.0\pm0.1$ ), J0121 ( $4.1\pm0.1$ ), UAS:bd1 ( $3.1\pm0.1$ ), UAS:BDL ( $2.8\pm0.1$ ) and J0121xUAS:BDL ( $3.6\pm0.1$ ) displayed no reduction in the number of lateral roots/cm (FIG. 6).

#### Example 10

##### Role of CYCA2;4 in Lateral Root Formation

CYCA2;4 was identified as a putative important regulator of cell division during lateral root initiation (Vanneste et al., 2005). However, overexpression of CYCA2;4 did not induce an increase in lateral roots (similar to overexpression of other cell cycle genes), while it did stimulate cell cycle progression as exemplified by a strong reduction of endoreduplication level in cotyledons. Also in knock-outs we did not observe obvious changes in lateral root density. But, CYCA2;4 belongs to a small gene family consisting of 4 members. Combining mutations in various members of this family did result in dramatic reductions of lateral root density (FIG. 7). Taken together these data suggest that A2-type cyclins are required, but not sufficient for lateral root initiation to occur.

Interestingly, CYCA2;4—a core cell cycle gene—is retained in the list of genes after meta-analysis. Unfortunately, the lack of lateral root phenotype in the overexpression lines might suggest that a combination of genes/factors is required to specifically drive asymmetric cell division and lateral root initiation. The most likely candidates that, when combined, will induce lateral root initiation are within the subset of 15 genes identified under example 8.

#### Example 11

##### Mutant Screening

A number of SALK T-DNA insertion mutants from genes in various clusters were made homozygous and analyzed for their lateral root phenotype (FIG. 8). In the graph, bars of mutants with a significant increase or decrease in the lateral root number are colored green or red, respectively. The green or red box around part of the graph indicates genes from up- or down regulated clusters respectively.

In addition to the lateral root phenotype, defects in other processes requiring asymmetric cell divisions were also detected, i.e. stomata formation and embryogenesis.

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#### Example 12

##### Expression Analysis by GUS/GFP Fusion

5 A number of promoter-GUS/GFP fusions from genes in various clusters were made homozygous and analyzed in detail for their expression pattern (FIG. 9). Mainly, the GFP expression pattern was in agreement with the up- or down regulation of the gene in micro array dataset.

10 For 4 genes the expression pattern was analyzed in detail, and revealed a specific up- or down regulation of the GUS/GFP in the lateral root initiation site at the time of asymmetric cell division in agreement with the transcript level detected in the micro array (FIG. 10).

15 Tables

TABLE 1

| Overview of shifts in functional categories after filtering |                               |           |          |
|---|-------------------------------|-----------|----------|
|   | Functional categories         | % in 3110 | % in 266 |
| 20  | Cell cycle/DNA synthesis      | 3.9       | 8.3      |
|   | Kinase/Phosphatase            | 5.5       | 3.4      |
|   | Metabolism/Energy             | 22.7      | 12.4     |
|   | Protein synthesis/degradation | 9.7       | 9.0      |
|   | RNA processing                | 1.6       | 3.0      |
|   | Signalling/development        | 6.8       | 12.8     |
|   | Stress                        | 4.0       | 2.3      |
|   | Transcriptional activity      | 10.9      | 14.7     |
|   | Transport                     | 7.2       | 2.3      |
|   | Other                         | 5.5       | 7.1      |
| 30  | Unclassified/unknown          | 22.1      | 24.4     |

Lateral root initiation encrypted in 'lateral root initiation' genes

TABLE 2

| List of up-regulated transcription factors that are not responsive in the mutant (slr) |                              |           |               |
|--|------------------------------|-----------|---------------|
| Cluster coordinates  |                              |           |               |
| AGI code   | Description                  | Wild-type | Solitary root |
| At2g33720  | ABI3/VP1-related TF          | 4         | 7             |
| At5g53290  | AP2 domain TF                | 1         | 4             |
| At4g23750  | AP2 domain TF                | 1         | 6             |
| At5g18560  | AP2 domain TF                | 1         | 8             |
| 45 At1g28360   | AP2 domain TF                | 2         | 8             |
| At5g10510  | AP2 domain TF                | 3         | 8             |
| At5g57390  | AP2 domain TF                | 3         | 8             |
| At4g28640  | Aux/IAA family (IAA11)       | 1         | 2             |
| At4g32280  | Aux/IAA family (IAA29)       | 1         | 2             |
| At3g62100  | Aux/IAA family (IAA30)       | 1         | 4             |
| 50 At5g43700   | Aux/IAA family (IAA4)        | 2         | 5             |
| At5g60450  | Auxin Response Factor (ARF4) | 2         | 8             |
| At4g00940  | DOF zinc finger protein      | 4         | 9             |
| At1g27050  | Homeobox TF                  | 2         | 7             |
| At2g01430  | Homeobox TF                  | 2         | 7             |
| At1g14350  | MYB domain TF (AtMYB124)     | 2         | 5             |
| At1g18570  | MYB domain TF (AtMYB51)      | 4         | 9             |
| 55 At2g47260   | WRKY domain TF (WRKY23)      | 3         | 7             |
| At5g26930  | GATA zinc finger protein     | 1         | 4             |

TABLE 3

| List of genes that are up-regulated in the xylem pole pericycle, that are not responsive in the slr mutant and that show potential involvement in the asymmetric cell division |   |  |
|--|---|--|
| AGI code   | Description   |  |
| AT5G63950  | SNF2 DOMAIN-CONTAINING PROTEIN/HELICASE DOMAIN-CONTAINING PROTEIN |  |

TABLE 3-continued

List of genes that are up-regulated in the xylem pole pericycle, that are not responsive in the slr mutant and that show potential involvement in the asymmetric cell division

| AGI code  | Description   |
|-----------|---|
| AT5G67100 | DNA-DIRECTED DNA POLYMERASE ALPHA CATALYTIC SUBUNIT, PUTATIVE         |
| AT2G33620 | DNA-BINDING FAMILY PROTEIN/AT-HOOK PROTEIN 1 (AHP1)                   |
| AT2G46990 | AUXIN-RESPONSIVE PROTEIN/INDOLEACETIC ACID-INDUCED PROTEIN 20 (IAA20) |
| AT5G47440 | EXPRESSED PROTEIN STRONG SIMILARITY TO UNKNOWN PROTEIN                |
| AT4G32460 | EXPRESSED PROTEIN   |
| AT4G13210 | PECTATE LYASE FAMILY PROTEIN  |
| AT3G59430 | EXPRESSED PROTEIN   |
| AT3G01070 | PLASTOCYANIN-LIKE DOMAIN-CONTAINING PROTEIN                           |
| AT3G59420 | RECEPTOR PROTEIN KINASE, PUTATIVE (ACR4)                              |
| AT1G80370 | CYCLIN, PUTATIVE  |
| AT1G69530 | EXPANSIN, PUTATIVE (EXP1)   |
| AT4G02060 | PROLIFERA PROTEIN (PRL)/DNA REPLICATION LICENSING FACTOR MCM7 (MCM7)  |
| AT5G67070 | RAPID ALKALINIZATION FACTOR (RALF) FAMILY PROTEIN                     |
| AT1G61580 | 60S RIBOSOMAL PROTEIN L3 (RPL3B)                                      |

TABLE 4

Expression in an early stage of genes involved in auxin signalling and transport as determined by the cell sorting approach.

| Gene Name(s) | agi       | 0 h      | 2 h      | 6 h      | 25 |
|--------------|-----------|----------|----------|----------|----|
| AAP6         | At5g49630 | 0.852584 | 1.25473  | 1.549922 |    |
| ALF1 SUR1    | AT2g20610 | 3.526627 | 1.659614 | 1.132184 |    |
| RTY          |           |          |          |          |    |
| ARF16        | At4g30080 | 0.727253 | 1.044252 | 1.222434 | 30 |
| ARF18        | At3g61830 | 1.02858  | 1.042211 | 1.37744  |    |
| ARF19        | At1g19220 | 0.964729 | 2.260746 | 1.345781 |    |
| AKF4         | At5g60450 | 0.993832 | 2.433736 | 1.34132  |    |
| ARF5 IAA24   | At1g19850 | 0.805484 | 1.062866 | 1.646489 |    |
| MP           |           |          |          |          |    |
| ATGH3_1      | At2g14960 | 0.993763 | 14.46607 | 12.64589 | 35 |
| ATGH3_4      | At1g59500 | 1.832319 | 11.94342 | 5.062107 |    |
| ATGH3_5      | AT4g27260 | 4.933415 | 36.44469 | 28.02028 |    |
| ATGH3_6 DFL1 | At5g54510 | 4.107676 | 33.98892 | 33.18595 |    |
| ATSAUR32     | At2g46690 | 0.745399 | 1.083697 | 1.357203 |    |
| ATSAUR51     | At1g75580 | 0.641888 | 0.861681 | 1.394927 |    |
| DFL1         | AT5G54510 | 4.107676 | 33.98892 | 33.18595 | 40 |
| HAT2         | AT5G47370 | 3.866166 | 5.905478 | 1.72286  |    |
| IAA1         | AT4G14560 | 1.444098 | 2.650251 | 3.498028 |    |
| IAA11        | AT4G28640 | 1.081115 | 2.990535 | 3.893183 |    |
| IAA12 BDL    | AT1G04550 | 1.070244 | 2.483024 | 2.141742 |    |
| IAA13        | AT2G33310 | 3.386846 | 16.95071 | 17.15706 |    |
| IAA17 AXR3   | AT1G04250 | 4.20049  | 5.560019 | 1.337217 | 45 |
| IAA19 MSG2   | AT3G15540 | 8.950041 | 37.74343 | 43.64249 |    |
| IAA20        | AT2G46990 | 0.643367 | 0.719127 | 1.830361 |    |
| IAA26 PAP1   | AT3G16500 | 1.67767  | 4.3412   | 2.185664 |    |
| IAA29        | AT4G32280 | 1.230655 | 15.62485 | 12.44667 |    |
| IAA3 SHY2    | AT1G04240 | 0.649735 | 1.143323 | 0.778411 |    |
| IAA5         | AT1G15580 | 0.800279 | 1.701733 | 2.127686 | 50 |
| PINOID-LIKE  | At3g44610 | 0.730512 | 0.863134 | 2.114596 |    |

TABLE 5

code of the mutants used

| Code on graph | AGI       |
|---------------|-----------|
| H19           | At3g59850 |
| R             | At4g23750 |
| S             | At4g23750 |
| H12           | At4g38210 |
| H10           | At5g15080 |
| 101           | At5g51560 |
| KO1           | At1g11140 |
| KO2           | At1g55580 |
| 90            | At1g57820 |

TABLE 5-continued

| code of the mutants used | 25 | Code on graph | AGI       |
|--------------------------|----|---------------|-----------|
|                          |    | H8            | At1g69530 |
|                          |    | 108           | At1g72250 |
|                          |    | H2            | At2g06850 |
|                          |    | 67            | At2g22610 |
|                          |    | 68            | At2g28620 |
|                          |    | 94            | At2g28620 |
|                          |    | 135           | AT2G33620 |
|                          |    | 59            | At3g51280 |
|                          |    | 87            | At3g51740 |
|                          |    | 105           | At3g53190 |
|                          |    | 83            | At4g02150 |
|                          |    | 85            | At4g05190 |
|                          |    | 105           | At4g18570 |
|                          |    | 91            | At4g21820 |
|                          |    | 111           | At4g29360 |
|                          |    | 75            | At4g32830 |
|                          |    | 106           | At4g32830 |
|                          |    | H23           | At5g08000 |
|                          |    | 88            | At5g45780 |
|                          |    | 124           | At5g47440 |
|                          |    | 65            | At5g48460 |
|                          |    | H3a           | At1g08840 |
|                          |    | M             | At1g72310 |
|                          |    | H4            | At1g75640 |
|                          |    | 5             | At4g28640 |
|                          |    | H15           | At1g64390 |
|                          |    | H20           | At3g58040 |
|                          |    | H21           | At1g14720 |
|                          |    | H6            | At1g29050 |
|                          |    | H29           | At1g53500 |
|                          |    | H1            | At1g06110 |
|                          |    | H26           | At2g45470 |
|                          |    | H28           | At3g10810 |
|                          |    | H5            | At3g52370 |
|                          |    | H18           | At4g03960 |
|                          |    | H9            | At4g14130 |
|                          |    | H27           | At5g18650 |
|                          |    | H13           | At5g38895 |
|                          |    | H17           | At5g54160 |
|                          |    | H16           | At5g57740 |
|                          |    | H22           | At5g03650 |
|                          |    | 6             | At2g33830 |
|                          |    | 22            | At2g33830 |
|                          |    | H7            | At3g54920 |
|                          |    | H24           | At3g54920 |

TABLE 6

genes used in GUS fusion

|    |   |
|----|---|
| 1  | pAt4g13770::GUS                           |
| 2  | pAT2G20610::GUS                           |
| 3  | pAt3g46130::GUS                           |
| 4  | pAt3g11280::GUS                           |
| 5  | pAt1g49740::GUS                           |
| 6  | pAt1g64405::GUS                           |
| 7  | pAt3g55620::GUS                           |
| 8  | pCYCB1;1::GUS                             |
| 9  | pCYCB1;3::GUS                             |
| 10 | pCYCB2;2::GUS                             |
| 11 | pCYCB2;4::GUS                             |
| 12 | pCYCA2;2::GUS                             |
| 13 | pCYCA2;3::GUS                             |
| 14 | pCDKB2;2::GUS                             |
| 15 | pCKS2::GUS                                |
| 16 | pDEL3::GUS                                |
| 17 | pAt3g58100::GUS                           |
| 18 | pAt1g54990::GUS                           |
| 19 | pAt5g26930::GUS                           |
| 20 | pAT1G69530::GUS                           |
| 21 | pACR4>>H2B::YFP<br>(Gifford et al., 2003) |

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| His | Asp | Glu | Ser | Ser | Glu | Asn | Ser | Lys | Lys | Ser | Leu | Val | Ser | Thr | Thr |
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 Lys Asp Pro Trp Ile Ile Lys Lys Val Phe His Phe Ala Ser Val Leu  
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 Phe Tyr Asp Lys Thr Trp Pro His Asp Pro Asn Val Ala Tyr Asn Lys  
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Gly Lys Ser Leu Lys Lys Val Ser Ile Cys Tyr Thr Asp Pro Asp Ala  
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|--|-----|-----|

|  |     |     |
|--|-----|-----|
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|  |     |     |
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|   |    |    |
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|   |    |    |
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|---|----|----|

|   |    |    |
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|   |    |    |    |
|---|----|----|----|
| Val Asp Pro Gln Ser His His Ser Gln Asn His Ile Pro Lys Leu Glu<br>65 | 70 | 75 | 80 |
|---|----|----|----|

|   |    |    |
|---|----|----|
| Asp Phe Leu Gly Asp Ser Ser Ile Val Arg Tyr Ser Asp Asn Ser<br>85 | 90 | 95 |
|---|----|----|

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|--|-----|-----|
| Gln Thr Asp Thr Gln Asp Ser Ser Leu Thr Gln Ile Tyr Asp Pro Arg<br>100 | 105 | 110 |
|--|-----|-----|

|  |     |     |
|--|-----|-----|
| His His His Asn Gln Thr Gly Phe Tyr Ser Asp His His Asp Phe Lys<br>115 | 120 | 125 |
|--|-----|-----|

|  |     |     |
|--|-----|-----|
| Thr Met Ala Gly Phe Gln Ser Ala Phe Ser Thr Asn Ser Gly Ser Glu<br>130 | 135 | 140 |
|--|-----|-----|

|  |     |     |     |
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|--|-----|-----|-----|

|  |     |     |
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|  |     |     |
|--|-----|-----|
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|--|-----|-----|

|  |     |     |
|--|-----|-----|
| Asn His Arg Asn Asp Asn Asn His Tyr Arg Gly Asn Asn Asn Gly<br>195 | 200 | 205 |
|--|-----|-----|

|  |     |     |
|--|-----|-----|
| Glu Arg Ile Asn Asn Asn Asn Asn Asn Asp Asn Glu Lys Thr Asp Ser<br>210 | 215 | 220 |
|--|-----|-----|

|  |     |     |     |
|--|-----|-----|-----|
| Glu Lys Glu Lys Ala Val Val Ala Val Glu Thr Ser Asp Cys Ser Asn<br>225 | 230 | 235 | 240 |
|--|-----|-----|-----|

|  |     |     |
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Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp  
260 265 270

Asn Ser Cys Arg Arg Glu Gly Gln Ala Arg Lys Gly Arg Gln Gly Gly  
275 280 285

Tyr Asp Lys Glu Asp Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu  
290 295 300

Lys Tyr Trp Asn Ala Thr Ala Thr Asn Phe Pro Ile Thr Asn Tyr  
305 310 315 320

Ser Lys Glu Val Glu Glu Met Lys His Met Thr Lys Gln Glu Phe Ile  
325 330 335

Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile  
340 345 350

Tyr Arg Gly Val Thr Arg His His Gln Gln Gly Arg Trp Gln Ala Arg  
355 360 365

Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ala  
370 375 380

Thr Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe  
385 390 395 400

Arg Gly Ile Asn Ala Val Thr Asn Phe Glu Met Asn Arg Tyr Asp Val  
405 410 415

Glu Ala Ile Met Lys Ser Ala Leu Pro Ile Gly Gly Ala Ala Lys Arg  
420 425 430

Leu Lys Leu Ser Leu Glu Ala Ala Ala Ser Ser Glu Gln Lys Pro Ile  
435 440 445

Leu Gly His His Gln Leu His His Phe Gln Gln Gln Gln Gln Gln  
450 455 460

Gln Leu Gln Leu Gln Ser Ser Pro Asn His Ser Ser Ile Asn Phe Ala  
465 470 475 480

Leu Cys Pro Asn Ser Ala Val Gln Ser Gln Gln Ile Ile Pro Cys Gly  
485 490 495

Ile Pro Phe Glu Ala Ala Ala Leu Tyr His His His Gln Gln Gln Gln  
500 505 510

Gln His Gln Gln Gln Gln Gln Gln Asn Phe Phe Gln His Phe Pro  
515 520 525

Ala Asn Ala Ala Ser Asp Ser Thr Gly Ser Asn Asn Asn Ser Asn Val  
530 535 540

Gln Gly Thr Met Gly Leu Met Ala Pro Asn Pro Ala Glu Phe Phe Leu  
545 550 555 560

Trp Pro Asn Gln Ser Tyr  
565

<210> SEQ\_ID NO 7  
<211> LENGTH: 555  
<212> TYPE: PRT  
<213> ORGANISM: Arabidopsis thaliana  
<220> FEATURE:  
<221> NAME/KEY: MISC\_FEATURE  
<223> OTHER INFORMATION: At5g57390

&lt;400&gt; SEQUENCE: 7

Met Lys Asn Asn Asn Asn Lys Ser Ser Ser Ser Ser Tyr Asp Ser  
1 5 10 15

Ser Leu Ser Pro Ser Ser Ser Ser Ser His Gln Asn Trp Leu Ser  
20 25 30

Phe Ser Leu Ser Asn Asn Asn Asn Asn Phe Asn Ser Ser Ser Asn Pro  
35 40 45

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Asn Leu Thr Ser Ser Thr Ser Asp His His His Pro His Pro Ser His  
 50 55 60  
 Leu Ser Leu Phe Gln Ala Phe Ser Thr Ser Pro Val Glu Arg Gln Asp  
 65 70 75 80  
 Gly Ser Pro Gly Val Ser Pro Ser Asp Ala Thr Ala Val Leu Ser Val  
 85 90 95  
 Tyr Pro Gly Gly Pro Lys Leu Glu Asn Phe Leu Gly Gly Ala Ser  
 100 105 110  
 Thr Thr Thr Arg Pro Met Gln Gln Val Gln Ser Leu Gly Gly Val  
 115 120 125  
 Val Phe Ser Ser Asp Leu Gln Pro Pro Leu His Pro Pro Ser Ala Ala  
 130 135 140  
 Glu Ile Tyr Asp Ser Glu Leu Lys Ser Ile Ala Ala Ser Phe Leu Gly  
 145 150 155 160  
 Asn Tyr Ser Gly Gly His Ser Ser Glu Val Ser Ser Val His Lys Gln  
 165 170 175  
 Gln Pro Asn Pro Leu Ala Val Ser Glu Ala Ser Pro Thr Pro Lys Lys  
 180 185 190  
 Asn Val Glu Ser Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr  
 195 200 205  
 Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser  
 210 215 220  
 Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln Gly Tyr Asp  
 225 230 235 240  
 Lys Glu Asp Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr  
 245 250 255  
 Trp Gly Pro Thr Thr Thr Asn Phe Pro Ile Ser Asn Tyr Glu Ser  
 260 265 270  
 Glu Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Phe Val Ala Ser  
 275 280 285  
 Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Met Tyr Arg  
 290 295 300  
 Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly  
 305 310 315 320  
 Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln  
 325 330 335  
 Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly  
 340 345 350  
 Leu Asn Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val Lys Ser  
 355 360 365  
 Ile Ala Ser Cys Asn Leu Pro Val Gly Gly Leu Met Pro Lys Pro Ser  
 370 375 380  
 Pro Ala Thr Ala Ala Ala Asp Lys Thr Val Asp Leu Ser Pro Ser Asp  
 385 390 395 400  
 Ser Pro Ser Leu Thr Thr Pro Ser Leu Thr Phe Asn Val Ala Thr Pro  
 405 410 415  
 Val Asn Asp His Gly Gly Thr Phe Tyr His Thr Gly Ile Pro Ile Lys  
 420 425 430  
 Pro Asp Pro Ala Asp His Tyr Trp Ser Asn Ile Phe Gly Phe Gln Ala  
 435 440 445  
 Asn Pro Lys Ala Glu Met Arg Pro Leu Ala Asn Phe Gly Ser Asp Leu  
 450 455 460

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His Asn Pro Ser Pro Gly Tyr Ala Ile Met Pro Val Met Gln Glu Gly  
465                    470                    475                    480

Glu Asn Asn Phe Gly Gly Ser Phe Val Gly Ser Asp Gly Tyr Asn Asn  
485                    490                    495

His Ser Ala Ala Ser Asn Pro Val Ser Ala Ile Pro Leu Ser Ser Thr  
500                    505                    510

Thr Thr Met Ser Asn Gly Asn Glu Gly Tyr Gly Gly Asn Ile Asn Trp  
515                    520                    525

Ile Asn Asn Asn Ile Ser Ser Ser Tyr Gln Thr Ala Lys Ser Asn Leu  
530                    535                    540

Ser Val Leu His Thr Pro Val Phe Gly Leu Glu  
545                    550                    555

<210> SEQ\_ID NO 8

<211> LENGTH: 246

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: MISC\_FEATURE

<223> OTHER INFORMATION: At4g28640

<400> SEQUENCE: 8

Met Glu Gly Gly Ser Ala Ser Gly Ser Ala Ser Ala Leu Ser Asn Asp  
1                    5                    10                    15

Glu Asn Leu Val Val Ser Cys Glu Asp Ser Ser Ser Pro Ile Gly Asn  
20                    25                    30

Glu Leu Glu Leu Gly Leu Thr Leu Ser Leu Gly Arg Lys Gly Tyr Arg  
35                    40                    45

Asp Cys Arg Val Tyr Ala Asp Asp Ser Ser Ser Ser Ser Ser Ser Ser  
50                    55                    60

Ser Leu Ser Arg Ala Ser Val Ile Ala Gly Ile Lys Arg Thr Ala Asp  
65                    70                    75                    80

Ser Met Ala Ala Thr Ser Gly Gln Val Val Gly Trp Pro Pro Ile Arg  
85                    90                    95

Thr Tyr Arg Met Asn Ser Met Val Asn Gln Ala Lys Ala Ser Ala Thr  
100                    105                    110

Glu Asp Pro Asn Leu Glu Ile Ser Gln Ala Val Asn Lys Asn Arg Ser  
115                    120                    125

Asp Ser Thr Lys Met Arg Asn Ser Met Phe Val Lys Val Thr Met Asp  
130                    135                    140

Gly Ile Pro Ile Gly Arg Lys Ile Asp Leu Asn Ala His Lys Cys Tyr  
145                    150                    155                    160

Glu Ser Leu Ser Asn Thr Leu Glu Met Phe Leu Lys Pro Lys Leu  
165                    170                    175

Gly Ser Arg Thr Leu Glu Thr Asp Gly His Met Glu Thr Pro Val Lys  
180                    185                    190

Ile Leu Pro Asp Gly Ser Ser Gly Leu Val Leu Thr Tyr Glu Asp Lys  
195                    200                    205

Glu Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Gly Met Phe Ile  
210                    215                    220

Gly Ser Val Arg Arg Leu Arg Ile Met Lys Thr Ser Glu Ala Thr Gly  
225                    230                    235                    240

Lys Ala Gln Met Ile Leu  
245

<210> SEQ\_ID NO 9

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<211> LENGTH: 251  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At4g32280

<400> SEQUENCE: 9

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Met Glu Leu Asp Leu Gly Leu Ser Leu Ser Pro His Lys Ser Ser Lys
1           5          10          15

Leu Gly Phe Asn Phe Asp Leu Asn Lys His Cys Ala Ile Glu Gly Ala
20          25          30

Ala Ser Cys Leu Gly Thr Glu Lys Leu Arg Phe Glu Ala Thr Phe Gly
35          40          45

Leu Gly Asn Val Glu Glu Asn Cys Tyr Met Pro Lys Gln Arg Leu Phe
50          55          60

Ala Leu Asn Gly Gln Pro Asn Glu Glu Asp Glu Asp Pro Leu Glu Ser
65          70          75          80

Glu Ser Ser Ile Val Tyr Asp Asp Glu Glu Glu Asn Ser Glu Val Val
85          90          95

Gly Trp Pro Pro Val Lys Thr Cys Met Ile Lys Tyr Gly Ser Tyr His
100         105         110

His Arg His Ile Arg Asn His His Cys Pro Tyr His His Arg Gly
115         120         125

Arg Arg Ile Thr Ala Met Asn Asn Asn Ile Ser Asn Pro Thr Thr Ala
130         135         140

Thr Val Gly Ser Ser Ser Ser Ser Ile Ser Ser Arg Ser Ser Met
145         150         155         160

Tyr Val Lys Val Lys Met Asp Gly Val Ala Ile Ala Arg Lys Val Asp
165         170         175

Ile Lys Leu Phe Asn Ser Tyr Glu Ser Leu Thr Asn Ser Leu Ile Thr
180         185         190

Met Phe Thr Glu Tyr Glu Asp Cys Asp Arg Glu Asp Thr Asn Tyr Thr
195         200         205

Phe Thr Phe Gln Gly Lys Glu Gly Asp Trp Leu Leu Arg Gly Asp Val
210         215         220

Thr Trp Lys Ile Phe Ala Glu Ser Val His Arg Ile Ser Ile Ile Arg
225         230         235         240

Asp Arg Pro Cys Ala Tyr Thr Arg Cys Leu Phe
245         250
  
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<210> SEQ ID NO 10  
 <211> LENGTH: 172  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At3g62100

<400> SEQUENCE: 10

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Met Gly Arg Gly Arg Ser Ser Ser Ser Ser Ser Ile Glu Ser Ser Cys
1           5          10          15

Lys Ser Asn Pro Phe Gly Val Ser Ser Ser Asn Thr Arg Asn Leu Ser
20          25          30

Thr Asp Leu Arg Leu Gly Leu Ser Phe Gly Ser Ser Ser Gly Gln Tyr
35          40          45

Tyr Asn Gly Gly Asp Asn His Glu Tyr Asp Gly Val Gly Ala Ala Glu
50          55          60
  
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Glu Met Met Ile Met Glu Glu Glu Gln Asn Glu Cys Asn Ser Val  
 65 70 75 80  
 Gly Ser Phe Tyr Val Lys Val Asn Met Glu Gly Val Pro Ile Gly Arg  
 85 90 95  
 Lys Ile Asp Leu Leu Ser Leu Asn Gly Tyr His Asp Leu Ile Thr Thr  
 100 105 110  
 Leu Asp Tyr Met Phe Asn Ala Ser Ile Leu Trp Ala Glu Glu Glu Asp  
 115 120 125  
 Met Cys Ser Glu Lys Ser His Val Leu Thr Tyr Ala Asp Lys Glu GLY  
 130 135 140  
 Asp Trp Met Met Val Gly Asp Val Pro Trp Glu Met Phe Leu Ser Ser  
 145 150 155 160  
 Val Arg Arg Leu Lys Ile Ser Arg Ala Tyr His Tyr  
 165 170

<210> SEQ ID NO 11  
 <211> LENGTH: 186  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At5g43700  
  
 <400> SEQUENCE: 11

Met Glu Lys Val Asp Val Tyr Asp Glu Leu Val Asn Leu Lys Ala Thr  
 1 5 10 15  
 Glu Leu Arg Leu Gly Leu Pro Gly Thr Glu Glu Thr Val Ser Cys Gly  
 20 25 30  
 Lys Ser Asn Lys Arg Val Leu Pro Glu Ala Thr Glu Lys Glu Ile Glu  
 35 40 45  
 Ser Thr Gly Lys Thr Glu Thr Ala Ser Pro Pro Lys Ala Gln Ile Val  
 50 55 60  
 Gly Trp Pro Pro Val Arg Ser Tyr Arg Lys Asn Asn Val Gln Thr Lys  
 65 70 75 80  
 Lys Ser Glu Ser Glu Gly Gln Gly Asn Tyr Val Lys Val Ser Met Asp  
 85 90 95  
 Gly Ala Pro Tyr Leu Arg Lys Ile Asp Leu Thr Met Tyr Lys Gln Tyr  
 100 105 110  
 Pro Glu Leu Met Lys Ser Leu Glu Asn Met Phe Lys Phe Ser Val Gly  
 115 120 125  
 Glu Tyr Phe Glu Arg Glu Gly Tyr Lys Gly Ser Asp Phe Val Pro Thr  
 130 135 140  
 Tyr Glu Asp Lys Asp Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp  
 145 150 155 160  
 Glu Met Phe Val Ser Ser Cys Lys Arg Leu Arg Ile Met Lys Gly Ser  
 165 170 175  
 Glu Val Lys Gly Leu Gly Cys Gly Gly Leu  
 180 185

<210> SEQ ID NO 12  
 <211> LENGTH: 788  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At5g60450  
  
 <400> SEQUENCE: 12

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Met Glu Phe Asp Leu Asn Thr Glu Ile Ala Glu Val Glu Glu Glu  
 1               5               10               15  
 Asn Asp Asp Val Gly Val Gly Gly Thr Arg Ile Asp Lys  
 20               25               30  
 Gly Arg Leu Gly Ile Ser Pro Ser Ser Ser Cys Ser Ser Gly  
 35               40               45  
 Ser Ser Ser Ser Ser Thr Gly Ser Ala Ser Ser Ile Tyr Ser  
 50               55               60  
 Glu Leu Trp His Ala Cys Ala Gly Pro Leu Thr Cys Leu Pro Lys Lys  
 65               70               75               80  
 Gly Asn Val Val Val Tyr Phe Pro Gln Gly His Leu Glu Gln Asp Ala  
 85               90               95  
 Met Val Ser Tyr Ser Ser Pro Leu Glu Ile Pro Lys Phe Asp Leu Asn  
 100              105              110  
 Pro Gln Ile Val Cys Arg Val Val Asn Val Gln Leu Leu Ala Asn Lys  
 115              120              125  
 Asp Thr Asp Glu Val Tyr Thr Gln Val Thr Leu Leu Pro Leu Gln Glu  
 130              135              140  
 Phe Ser Met Leu Asn Gly Glu Gly Lys Glu Val Lys Glu Leu Gly Gly  
 145              150              155              160  
 Glu Glu Glu Arg Asn Gly Ser Ser Ser Val Lys Arg Thr Pro His Met  
 165              170              175  
 Phe Cys Lys Thr Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe  
 180              185              190  
 Ser Val Pro Arg Arg Ala Ala Glu Asp Cys Phe Ala Pro Leu Asp Tyr  
 195              200              205  
 Lys Gln Gln Arg Pro Ser Gln Glu Leu Ile Ala Lys Asp Leu His Gly  
 210              215              220  
 Val Glu Trp Lys Phe Arg His Ile Tyr Arg Gly Gln Pro Arg Arg His  
 225              230              235              240  
 Leu Leu Thr Thr Gly Trp Ser Ile Phe Val Ser Gln Lys Asn Leu Val  
 245              250              255  
 Ser Gly Asp Ala Val Leu Phe Leu Arg Asp Glu Gly Gly Glu Leu Arg  
 260              265              270  
 Leu Gly Ile Arg Arg Ala Ala Arg Pro Arg Asn Gly Leu Pro Asp Ser  
 275              280              285  
 Ile Ile Glu Lys Asn Ser Cys Ser Asn Ile Leu Ser Leu Val Ala Asn  
 290              295              300  
 Ala Val Ser Thr Lys Ser Met Phe His Val Phe Tyr Ser Pro Arg Ala  
 305              310              315              320  
 Thr His Ala Glu Phe Val Ile Pro Tyr Glu Lys Tyr Ile Thr Ser Ile  
 325              330              335  
 Arg Ser Pro Val Cys Ile Gly Thr Arg Phe Arg Met Arg Phe Glu Met  
 340              345              350  
 Asp Asp Ser Pro Glu Arg Arg Cys Ala Gly Val Val Thr Gly Val Cys  
 355              360              365  
 Asp Leu Asp Pro Tyr Arg Trp Pro Asn Ser Lys Trp Arg Cys Leu Leu  
 370              375              380  
 Val Arg Trp Asp Glu Ser Phe Val Ser Asp His Gln Glu Arg Val Ser  
 385              390              395              400  
 Pro Trp Glu Ile Asp Pro Ser Val Ser Leu Pro His Leu Ser Ile Gln  
 405              410              415

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Ser Ser Pro Arg Pro Lys Arg Pro Trp Ala Gly Leu Leu Asp Thr Thr  
 420 425 430  
 Pro Pro Gly Asn Pro Ile Thr Lys Arg Gly Gly Phe Leu Asp Phe Glu  
 435 440 445  
 Glu Ser Val Arg Pro Ser Lys Val Leu Gln Gly Gln Glu Asn Ile Gly  
 450 455 460  
 Ser Ala Ser Pro Ser Gln Gly Phe Asp Val Met Asn Arg Arg Ile Leu  
 465 470 475 480  
 Asp Phe Ala Met Gln Ser His Ala Asn Pro Val Leu Val Ser Ser Arg  
 485 490 495  
 Val Lys Asp Arg Phe Gly Glu Phe Val Asp Ala Thr Gly Val Asn Pro  
 500 505 510  
 Ala Cys Ser Gly Val Met Asp Leu Asp Arg Phe Pro Arg Val Leu Gln  
 515 520 525  
 Gly Gln Glu Ile Cys Ser Leu Lys Ser Phe Pro Gln Phe Ala Gly Phe  
 530 535 540  
 Ser Pro Ala Ala Ala Pro Asn Pro Phe Ala Tyr Gln Ala Asn Lys Ser  
 545 550 555 560  
 Ser Tyr Tyr Pro Leu Ala Leu His Gly Ile Arg Ser Thr His Val Pro  
 565 570 575  
 Tyr Gln Asn Pro Tyr Asn Ala Gly Asn Gln Ser Ser Gly Pro Pro Ser  
 580 585 590  
 Arg Ala Ile Asn Phe Gly Glu Glu Thr Arg Lys Phe Asp Ala Gln Asn  
 595 600 605  
 Glu Gly Gly Leu Pro Asn Asn Val Thr Ala Asp Leu Pro Phe Lys Ile  
 610 615 620  
 Asp Met Met Gly Lys Gln Lys Gly Ser Glu Leu Asn Met Asn Ala Ser  
 625 630 635 640  
 Ser Gly Cys Lys Leu Phe Gly Phe Ser Leu Pro Val Glu Thr Pro Ala  
 645 650 655  
 Ser Lys Pro Gln Ser Ser Ser Lys Arg Ile Cys Thr Lys Val His Lys  
 660 665 670  
 Gln Gly Ser Gln Val Gly Arg Ala Ile Asp Leu Ser Arg Leu Asn Gly  
 675 680 685  
 Tyr Asp Asp Leu Leu Met Glu Leu Glu Arg Leu Phe Asn Met Glu Gly  
 690 695 700  
 Leu Leu Arg Asp Pro Glu Lys Gly Trp Arg Ile Leu Tyr Thr Asp Ser  
 705 710 715 720  
 Glu Asn Asp Met Met Val Val Gly Asp Asp Pro Trp His Asp Phe Cys  
 725 730 735  
 Asn Val Val Trp Lys Ile His Leu Tyr Thr Lys Glu Glu Val Glu Asn  
 740 745 750  
 Ala Asn Asp Asp Asn Lys Ser Cys Leu Glu Gln Ala Ala Leu Met Met  
 755 760 765  
 Glu Ala Ser Lys Ser Ser Ser Val Ser Gln Pro Asp Ser Ser Pro Thr  
 770 775 780  
 Ile Thr Arg Val  
 785

<210> SEQ ID NO 13  
 <211> LENGTH: 294  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE

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&lt;223&gt; OTHER INFORMATION: At4g00940

&lt;400&gt; SEQUENCE: 13

Met Asp His His Gln Tyr His His Asp Gln Tyr Gln His Gln Met  
 1                   5                   10                   15

Met Thr Ser Thr Asn Asn Asn Ser Tyr Asn Thr Ile Val Thr Thr Gln  
 20                 25                   30

Pro Pro Pro Thr Thr Thr Met Asp Ser Thr Thr Ala Thr Thr Met  
 35                 40                   45

Ile Met Asp Asp Glu Lys Lys Leu Met Thr Thr Met Ser Thr Arg Pro  
 50                 55                   60

Gln Glu Pro Arg Asn Cys Pro Arg Cys Asn Ser Ser Asn Thr Lys Phe  
 65                 70                   75                   80

Cys Tyr Tyr Asn Asn Tyr Ser Leu Ala Gln Pro Arg Tyr Leu Cys Lys  
 85                 90                   95

Ser Cys Arg Arg Tyr Trp Thr Glu Gly Gly Ser Leu Arg Asn Val Pro  
 100               105                   110

Val Gly Gly Gly Ser Arg Lys Asn Lys Lys Leu Pro Phe Pro Asn Ser  
 115               120                   125

Ser Thr Ser Ser Ser Thr Lys Asn Leu Pro Asp Leu Asn Pro Pro Phe  
 130               135                   140

Val Phe Thr Ser Ser Ala Ser Ser Asn Pro Ser Lys Thr His Gln  
 145               150                   155                   160

Asn Asn Asn Asp Leu Ser Leu Ser Phe Ser Ser Pro Met Gln Asp Lys  
 165               170                   175

Arg Ala Gln Gly His Tyr Gly His Phe Ser Glu Gln Val Val Thr Gly  
 180               185                   190

Gly Gln Asn Cys Leu Phe Gln Ala Pro Met Gly Met Ile Gln Phe Arg  
 195               200                   205

Gln Glu Tyr Asp His Glu His Pro Lys Lys Asn Leu Gly Phe Ser Leu  
 210               215                   220

Asp Arg Asn Glu Glu Ile Gly Asn His Asp Asn Phe Val Val Asn  
 225               230                   235                   240

Glu Glu Gly Ser Lys Met Met Tyr Pro Tyr Gly Asp His Glu Asp Arg  
 245               250                   255

Gln Gln His His His Val Arg His Asp Asp Gly Asn Lys Lys Arg Glu  
 260               265                   270

Gly Gly Ser Ser Asn Glu Leu Trp Ser Gly Ile Ile Leu Gly Gly Asp  
 275               280                   285

Ser Gly Gly Pro Thr Trp  
 290

&lt;210&gt; SEQ\_ID NO 14

&lt;211&gt; LENGTH: 444

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: MISC\_FEATURE

&lt;223&gt; OTHER INFORMATION: At1g27050

&lt;400&gt; SEQUENCE: 14

Met Asp Glu Glu Asp Val Cys Glu Ser Tyr Met Met Arg Glu Ile Thr  
 1                 5                   10                   15

Lys Lys Arg Lys Leu Thr Pro Ile Gln Leu Arg Leu Leu Glu Glu Ser  
 20                25                   30

Phe Glu Glu Lys Arg Leu Glu Pro Asp Arg Lys Leu Trp Leu Ala

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|   |     |     |
|---|-----|-----|
| 35  | 40  | 45  |
| Glu Lys Leu Gly Leu Gln Pro Ser Gln Val Ala Val Trp Phe Gln Asn |     |     |
| 50  | 55  | 60  |
| Arg Arg Ala Arg Tyr Lys Thr Lys Gln Leu Glu His Asp Cys Asp Ser |     |     |
| 65  | 70  | 75  |
| Leu Lys Ala Ser Tyr Ala Lys Leu Lys Thr Asp Trp Asp Ile Leu Phe |     |     |
| 85  | 90  | 95  |
| Val Gln Asn Gln Thr Leu Lys Ser Lys Val Gln Phe Leu Asn Arg Leu |     |     |
| 100   | 105 | 110 |
| Thr Ser His Tyr Phe Gln Glu Ser Val Gln Asn Phe Asp Asp Thr Phe |     |     |
| 115   | 120 | 125 |
| Lys Gln Val Asp Leu Leu Lys Glu Lys Leu Lys Met Gln Glu Asn Leu |     |     |
| 130   | 135 | 140 |
| Glu Thr Gln Ser Ile Glu Arg Lys Arg Leu Gly Glu Glu Gly Ser Ser |     |     |
| 145   | 150 | 155 |
| Val Lys Ser Asp Asn Thr Gln Tyr Ser Glu Glu Glu Gly Leu Glu Asn |     |     |
| 165   | 170 | 175 |
| Gln Tyr Ser Phe Pro Glu Leu Ala Val Leu Gly Phe Tyr Tyr Asp Pro |     |     |
| 180   | 185 | 190 |
| Thr Leu Thr Ala Ser Asn Leu Arg Gln Glu Pro Leu Lys Val Thr Cys |     |     |
| 195   | 200 | 205 |
| Ala Asp Gln Met Thr Gln Ile Gln Ile Ser Asp Val Thr Glu Pro Ala |     |     |
| 210   | 215 | 220 |
| Ser Ser Ala His Lys Lys Ile Glu Val Thr Gln Arg Ser Ser Ser Met |     |     |
| 225   | 230 | 235 |
| Ser Arg Lys Arg Asp Lys Pro Tyr Thr Asn Arg His Thr Pro Ala Arg |     |     |
| 245   | 250 | 255 |
| Ile Ser Lys Arg Arg Pro Trp Ala Pro Ser Ser Glu His Asp         |     |     |
| 260   | 265 | 270 |
| Glu Ile Ile Asp Lys Pro Ile Thr Lys Pro Pro Pro Pro Ala Leu     |     |     |
| 275   | 280 | 285 |
| Val Val Met Gly Leu Pro Ala Asn Cys Ser Val Leu Glu Leu Lys Ser |     |     |
| 290   | 295 | 300 |
| Arg Phe Glu Ile Tyr Gly Ser Ile Ser Arg Ile Arg Ile His Lys Asp |     |     |
| 305   | 310 | 315 |
| Gly Ile Gly Ser Val Ser Tyr Arg Thr Ala Glu Ser Ala Glu Ala Ala |     |     |
| 325   | 330 | 335 |
| Ile Ala Gly Ser His Glu Pro Ser Phe Gly Ile Ser Ile Asp Ser Lys |     |     |
| 340   | 345 | 350 |
| Lys Leu Glu Val Val Trp Ala Thr Asp Pro Leu Val Lys Trp Lys Glu |     |     |
| 355   | 360 | 365 |
| Gly Val Thr Ala Gly Glu Gly Lys Glu Arg Thr Ser Ser Phe Ser Ser |     |     |
| 370   | 375 | 380 |
| Lys Leu Leu Arg Pro Val Met Pro Leu Arg Lys His Gly Arg Ser Ser |     |     |
| 385   | 390 | 395 |
| Arg Leu Ala Ser Ala Ile Val Asn Pro Arg Ser Asp Asn Thr Lys Gly |     |     |
| 405   | 410 | 415 |
| Ile Ser Gly Asp Gly Gly Ile Ser Ser Pro Ala Thr Thr Ser Glu Val |     |     |
| 420   | 425 | 430 |
| Lys Gln Arg Asn Ile Val Thr Tyr Asp Asp Ile Val                 |     |     |
| 435   | 440 |     |

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<211> LENGTH: 275  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At2g01430

<400> SEQUENCE: 15

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Met Ile Lys Leu Leu Phe Thr Tyr Ile Cys Thr Tyr Thr Tyr Lys Leu
1           5          10          15

Tyr Ala Leu Tyr His Met Asp Tyr Ala Cys Val Cys Met Tyr Lys Tyr
20          25          30

Lys Gly Ile Val Thr Leu Gln Val Cys Leu Phe Tyr Ile Lys Leu Arg
35          40          45

Val Phe Leu Ser Asn Phe Thr Phe Ser Ser Ser Ile Leu Ala Leu Lys
50          55          60

Asn Pro Asn Asn Ser Leu Ile Lys Ile Met Ala Ile Leu Pro Glu Asn
65          70          75          80

Ser Ser Asn Leu Asp Leu Thr Ile Ser Val Pro Gly Phe Ser Ser Ser
85          90          95

Pro Leu Ser Asp Glu Gly Ser Gly Gly Arg Asp Gln Leu Arg Leu
100         105         110

Asp Met Asn Arg Leu Pro Ser Ser Glu Asp Gly Asp Asp Glu Glu Phe
115         120         125

Ser His Asp Asp Gly Ser Ala Pro Pro Arg Lys Lys Leu Arg Leu Thr
130         135         140

Arg Glu Gln Ser Arg Leu Leu Glu Asp Ser Phe Arg Gln Asn His Thr
145         150         155         160

Leu Asn Pro Lys Gln Lys Glu Val Leu Ala Lys His Leu Met Leu Arg
165         170         175

Pro Arg Gln Ile Glu Val Trp Phe Gln Asn Arg Arg Ala Arg Ser Lys
180         185         190

Leu Lys Gln Thr Glu Met Glu Cys Glu Tyr Leu Lys Arg Trp Phe Gly
195         200         205

Ser Leu Thr Glu Glu Asn His Arg Leu His Arg Glu Val Glu Glu Leu
210         215         220

Arg Ala Met Lys Val Gly Pro Thr Thr Val Asn Ser Ala Ser Ser Leu
225         230         235         240

Thr Met Cys Pro Arg Cys Glu Arg Val Thr Pro Ala Ala Ser Pro Ser
245         250         255

Arg Ala Val Val Pro Val Pro Ala Lys Lys Thr Phe Pro Pro Gln Glu
260         265         270

Arg Asp Arg
275
  
```

<210> SEQ\_ID NO 16  
 <211> LENGTH: 436  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At1g14350

<400> SEQUENCE: 16

```

Met Glu Asp Thr Lys Lys Lys Lys Lys Asn Ile Asn Asn Asn Gln
1           5          10          15

Asp Ser Lys Lys Lys Glu Arg His Ile Val Thr Trp Ser Gln Glu Glu
20          25          30
  
```

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Asp Val Ile Leu Arg Glu Gln Ile Thr Leu His Gly Thr Glu Asn Trp  
35 40 45

Ala Ile Ile Ala Ser Lys Phe Lys Asp Lys Ser Thr Arg Gln Cys Arg  
50 55 60

Arg Arg Trp Tyr Thr Tyr Leu Asn Ser Asp Phe Lys Arg Gly Gly Trp  
65 70 75 80

Ser Pro Glu Glu Asp Met Leu Leu Cys Glu Ala Gln Arg Val Phe Gly  
85 90 95

Asn Arg Trp Thr Glu Ile Ala Lys Val Val Ser Gly Arg Thr Asp Asn  
100 105 110

Ala Val Lys Asn Arg Phe Thr Thr Leu Cys Lys Lys Arg Ala Lys His  
115 120 125

Glu Ala Met Thr Lys Asp Ser Asn Ser Asn Thr Lys Arg Met Leu Phe  
130 135 140

Leu Asp Gly Ile Ser Thr Pro Arg Lys Ser Glu Asn Glu Thr Pro Ile  
145 150 155 160

Ala Lys Lys Leu Lys Arg Ser His Ile Leu Asp Leu Thr Glu Ile Ser  
165 170 175

Asn Tyr Gly Arg Ala Glu Ala Cys Val Asn Gln Gln Ile Arg Ser Pro  
180 185 190

Phe Ser Val Leu Ala Arg Asn Ala Thr Gly Ile Asp Ser Leu Glu Glu  
195 200 205

Gln Asn Gln Thr Ser Asn Val Asn Glu Ser Asp Gly Glu Gly Met Phe  
210 215 220

Leu Lys Lys Asp Asp Pro Lys Val Thr Ala Leu Met Gln Gln Ala Glu  
225 230 235 240

Leu Leu Ser Ser Leu Ala Gln Lys Val Asn Ala Asp Asn Thr Glu Gln  
245 250 255

Ser Met Glu Asn Ala Trp Lys Val Leu Gln Asp Phe Leu Asn Lys Gly  
260 265 270

Lys Glu Asn Asp Leu Phe Arg Tyr Gly Ile Pro Asp Ile Asp Phe Lys  
275 280 285

Ile Glu Glu Phe Lys Asp Leu Ile Glu Asp Leu Arg Ser Gly Tyr Glu  
290 295 300

Asp Asn Gln Leu Ser Trp Arg Gln Pro Asp Leu His Asp Ser Pro Ala  
305 310 315 320

Ser Ser Glu Tyr Ser Ser Gly Ser Thr Ile Met Val Asp Gln Ser Gly  
325 330 335

Asp Lys Thr Gln Pro Phe Ser Ala Asp Thr Gln Thr Glu His Lys Gln  
340 345 350

Val Gly Glu Glu Leu Leu Val Pro Lys Asn Pro Asp Glu Asn Met Pro  
355 360 365

Ile Ser Gly Glu Glu Lys Phe Ser Ser Pro Ile Gln Val Thr Pro Leu  
370 375 380

Phe Arg Ser Leu Ala Asp Gly Ile Pro Ser Pro Gln Phe Ser Glu Ser  
385 390 395 400

Glu Arg Ser Phe Leu Leu Lys Thr Leu Gly Ile Glu Ser Ser Ser Pro  
405 410 415

Cys Pro Ser Ala Asn Pro Ser Lys Pro Pro Pro Cys Lys Arg Val Leu  
420 425 430

Leu His Ser Leu  
435

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<210> SEQ ID NO 17
<211> LENGTH: 352
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: At1g18570

<400> SEQUENCE: 17

Met Val Arg Thr Pro Cys Cys Lys Ala Glu Leu Gly Leu Lys Lys Gly
1           5          10          15

Ala Trp Thr Pro Glu Glu Asp Gln Lys Leu Leu Ser Tyr Leu Asn Arg
20          25          30

His Gly Glu Gly Gly Trp Arg Thr Leu Pro Glu Lys Ala Gly Leu Lys
35          40          45

Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ala Asn Tyr Leu Arg Pro
50          55          60

Asp Ile Lys Arg Gly Glu Phe Thr Glu Asp Glu Glu Arg Ser Ile Ile
65          70          75          80

Ser Leu His Ala Leu His Gly Asn Lys Trp Ser Ala Ile Ala Arg Gly
85          90          95

Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
100         105         110

Ile Lys Lys Arg Leu Ile Lys Lys Gly Ile Asp Pro Val Thr His Lys
115         120         125

Gly Ile Thr Ser Gly Thr Asp Lys Ser Glu Asn Leu Pro Glu Lys Gln
130         135         140

Asn Val Asn Leu Thr Thr Ser Asp His Asp Leu Asp Asn Asp Lys Ala
145         150         155         160

Lys Lys Asn Asn Lys Asn Phe Gly Leu Ser Ser Ala Ser Phe Leu Asn
165         170         175

Lys Val Ala Asn Arg Phe Gly Lys Arg Ile Asn Gln Ser Val Leu Ser
180         185         190

Glu Ile Ile Gly Ser Gly Gly Pro Leu Ala Ser Thr Ser His Thr Thr
195         200         205

Asn Thr Thr Thr Ser Val Ser Val Asp Ser Glu Ser Val Lys Ser
210         215         220

Thr Ser Ser Ser Phe Ala Pro Thr Ser Asn Leu Leu Cys His Gly Thr
225         230         235         240

Val Ala Thr Thr Pro Val Ser Ser Asn Phe Asp Val Asp Gly Asn Val
245         250         255

Asn Leu Thr Cys Ser Ser Ser Thr Phe Ser Asp Ser Ser Val Asn Asn
260         265         270

Pro Leu Met Tyr Cys Asp Asn Phe Val Gly Asn Asn Asn Val Asp Asp
275         280         285

Glu Asp Thr Ile Gly Phe Ser Thr Phe Leu Asn Asp Glu Asp Phe Met
290         295         300

Met Leu Glu Glu Ser Cys Val Glu Asn Thr Ala Phe Met Lys Glu Leu
305         310         315         320

Thr Arg Phe Leu His Glu Asp Glu Asn Asp Val Val Asp Val Thr Pro
325         330         335

Val Tyr Glu Arg Gln Asp Leu Phe Asp Glu Ile Asp Asn Tyr Phe Gly
340         345         350

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&lt;210&gt; SEQ ID NO 18

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<211> LENGTH: 337  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At2g47260

<400> SEQUENCE: 18

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Met Glu Phe Thr Asp Phe Ser Lys Thr Ser Phe Tyr Tyr Pro Ser Ser
1           5          10          15

Gln Ser Val Trp Asp Phe Gly Asp Leu Ala Ala Ala Glu Arg His Ser
20          25          30

Leu Gly Phe Met Glu Leu Leu Ser Ser Gln Gln His Gln Asp Phe Ala
35          40          45

Thr Val Ser Pro His Ser Phe Leu Leu Gln Thr Ser Gln Pro Gln Thr
50          55          60

Gln Thr Gln Pro Ser Ala Lys Leu Ser Ser Ser Ile Ile Gln Ala Pro
65          70          75          80

Pro Ser Glu Gln Leu Val Thr Ser Lys Val Glu Ser Leu Cys Ser Asp
85          90          95

His Leu Leu Ile Asn Pro Pro Ala Thr Pro Asn Ser Ser Ser Ile Ser
100         105         110

Ser Ala Ser Ser Glu Ala Leu Asn Glu Glu Lys Pro Lys Thr Glu Asp
115         120         125

Asn Glu Glu Glu Gly Gly Glu Asp Gln Gln Glu Lys Ser His Thr Lys
130         135         140

Lys Gln Leu Lys Ala Lys Lys Asn Asn Gln Lys Arg Gln Arg Glu Ala
145         150         155         160

Arg Val Ala Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly
165         170         175

Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Phe
180         185         190

Pro Arg Ser Tyr Tyr Arg Cys Thr Thr Ala Ser Cys Asn Val Lys Lys
195         200         205

Arg Val Glu Arg Ser Phe Arg Asp Pro Ser Thr Val Val Thr Thr Tyr
210         215         220

Glu Gly Gln His Thr His Ile Ser Pro Leu Thr Ser Arg Pro Ile Ser
225         230         235         240

Thr Gly Gly Phe Phe Gly Ser Ser Gly Ala Ala Ser Ser Leu Gly Asn
245         250         255

Gly Cys Phe Gly Phe Pro Ile Asp Gly Ser Thr Leu Ile Ser Pro Gln
260         265         270

Phe Gln Gln Leu Val Gln Tyr His His Gln Gln Gln Gln Glu Leu
275         280         285

Met Ser Cys Phe Gly Gly Val Asn Glu Tyr Leu Asn Ser His Ala Asn
290         295         300

Glu Tyr Gly Asp Asp Asn Arg Val Lys Lys Ser Arg Val Leu Val Lys
305         310         315         320

Asp Asn Gly Leu Leu Gln Asp Val Val Pro Ser His Met Leu Lys Glu
325         330         335
  
```

Glu

<210> SEQ ID NO 19  
 <211> LENGTH: 120  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana

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<220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At5g26930

<400> SEQUENCE: 19

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Pro | Arg | Lys | Leu | Leu | Ser | Cys | Ser | Ser | Ser | Tyr | Val | Ser | Val |
| 1   |     |     |     | 5   |     |     | 10  |     |     |     |     | 15  |     |     |     |

Arg Met Lys Glu Glu Lys Gly Thr Ile Arg Cys Cys Ser Glu Cys Lys  
 20 25 30

Thr Thr Lys Thr Pro Met Trp Arg Gly Gly Pro Thr Gly Pro Lys Ser  
 35 40 45

Leu Cys Asn Ala Cys Gly Ile Arg His Arg Lys Gln Arg Arg Ser Glu  
 50 55 60

Leu Leu Gly Ile His Ile Ile Arg Ser His Lys Ser Leu Ala Ser Lys  
 65 70 75 80

Lys Ile Asn Leu Leu Ser Ser His Gly Gly Val Ala Val Lys Lys  
 85 90 95

Arg Arg Ser Leu Lys Glu Glu Gln Ala Ala Leu Cys Leu Leu Leu  
 100 105 110

Leu Ser Cys Ser Ser Val Leu Ala  
 115 120

<210> SEQ\_ID NO 20  
 <211> LENGTH: 1090  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At5G63950

<400> SEQUENCE: 20

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Asn | Thr | Ala | Ser | His | Arg | Arg | Lys | Pro | Arg | Ser | Leu | Asn |
| 1   |     |     |     |     | 5   |     | 10  |     |     | 15  |     |     |     |     |     |

Asp Arg His Tyr Ser Ile Leu Gln Asp Leu Ser Ala Pro Pro Arg Gln  
 20 25 30

Pro Pro Ser Ser Ser His Gly Glu Asp Glu Glu Thr Lys Lys Ser Met  
 35 40 45

Ile Lys Leu Ala Gly Arg Arg Leu Cys Lys Ala Leu Pro Lys Glu  
 50 55 60

Asp Glu Ala Asp Gly Tyr Asp Asp Pro Asp Leu Val Asp Phe Tyr Ser  
 65 70 75 80

Pro Val Lys Gly Glu Thr Ser Leu Asp Ser Ala Gly Ile Gly Asn Lys  
 85 90 95

Phe Thr Ser Trp Asp Glu Ser Lys Glu Ala Asn Thr Glu Leu Ala Gly  
 100 105 110

Glu Pro Asn Phe Ser Ile Ile Thr Asp Phe Cys Ser Pro Ser Pro Gln  
 115 120 125

Leu Lys Gln Lys Glu Glu Met Gln Gly Asp Gly Gly Arg Asn Glu Ile  
 130 135 140

Met Gly Ile Leu Asp Asp Leu Thr Ser Lys Leu Gly Thr Met Ser Ile  
 145 150 155 160

Gln Lys Lys Asp Ser Gln Ser Asn Asp Phe Asp Ala Cys Gly Val  
 165 170 175

Lys Ser Gln Val Asp Lys Phe Asp Phe Glu Asp Ala Lys Ser Ser Phe  
 180 185 190

Ser Leu Leu Ser Asp Leu Ser Lys Ser Ser Pro Asp Val Val Thr Thr  
 195 200 205

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Tyr Asn Ala Gly Val Asn Ser Ile Lys Asp Lys Gln Gly Lys Ser Gly  
210 215 220

Phe Ala Ile Arg Glu Glu Gln Thr Ser Lys Glu Phe Ser Arg Glu Trp  
225 230 235 240

Glu Glu Arg Ile Ser Asn Val Gly Lys Gln Asn Ser Tyr Ser Gly Arg  
245 250 255

His Phe Asp Asp Asn Ser Glu Asp Asn Arg Gln Gly Tyr Asn Leu Asp  
260 265 270

Arg Gly Lys Ser Gln Cys Lys Glu Val Asp Gln Ser Met Lys Thr Thr  
275 280 285

Arg His Ile Glu Val Ser Glu Lys Ile Arg Thr Val Gly Arg Ser Asn  
290 295 300

Ala Ala Lys Leu Arg Asp Leu Asp Glu Asp Asp Asp Asp Asp Cys  
305 310 315 320

Leu Ile Leu Ser Gly Lys Ala Ala Glu Met Lys Ile Asn Lys Pro  
325 330 335

Ala Arg Ser Tyr Asn Ala Lys Arg His Gly Tyr Asp Glu Arg Ser Leu  
340 345 350

Glu Asp Glu Gly Ser Ile Thr Leu Thr Gly Leu Asn Leu Ser Tyr Thr  
355 360 365

Leu Pro Gly Lys Ile Ala Thr Met Leu Tyr Pro His Gln Arg Glu Gly  
370 375 380

Leu Asn Trp Leu Trp Ser Leu His Thr Gln Gly Lys Gly Ile Leu  
385 390 395 400

Gly Asp Asp Met Gly Leu Gly Lys Thr Met Gln Ile Cys Ser Phe Leu  
405 410 415

Ala Gly Leu Phe His Ser Lys Leu Ile Lys Arg Ala Leu Val Val Ala  
420 425 430

Pro Lys Thr Leu Leu Pro His Trp Met Lys Glu Leu Ala Thr Val Gly  
435 440 445

Leu Ser Gln Met Thr Arg Glu Tyr Tyr Gly Thr Ser Thr Lys Ala Arg  
450 455 460

Glu Tyr Asp Leu His His Ile Leu Gln Gly Lys Gly Ile Leu Leu Thr  
465 470 475 480

Thr Tyr Asp Ile Val Arg Asn Asn Thr Lys Ala Leu Gln Gly Asp Asp  
485 490 495

His Tyr Thr Asp Glu Asp Asp Glu Asp Gly Asn Lys Trp Asp Tyr Met  
500 505 510

Ile Leu Asp Glu Gly His Leu Ile Lys Asn Pro Asn Thr Gln Arg Ala  
515 520 525

Lys Ser Leu Leu Glu Ile Pro Ser Ser His Arg Ile Ile Ile Ser Gly  
530 535 540

Thr Pro Ile Gln Asn Asn Leu Lys Glu Leu Trp Ala Leu Phe Asn Phe  
545 550 555 560

Ser Cys Pro Gly Leu Leu Gly Asp Lys Asn Trp Phe Lys Gln Asn Tyr  
565 570 575

Glu His Tyr Ile Leu Arg Gly Thr Asp Lys Asn Ala Thr Asp Arg Glu  
580 585 590

Gln Arg Ile Gly Ser Thr Val Ala Lys Asn Leu Arg Glu His Ile Gln  
595 600 605

Pro Phe Phe Leu Arg Arg Leu Lys Ser Glu Val Phe Gly Asp Asp Gly  
610 615 620

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**59****60**

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Ala Thr Ser Lys Leu Ser Lys Lys Asp Glu Ile Val Val Trp Leu Arg  
 625 630 635 640  
 Leu Thr Ala Cys Gln Arg Gln Leu Tyr Glu Ala Phe Leu Asn Ser Glu  
 645 650 655  
 Ile Val Leu Ser Ala Phe Asp Gly Ser Pro Leu Ala Ala Leu Thr Ile  
 660 665 670  
 Leu Lys Lys Ile Cys Asp His Pro Leu Leu Leu Thr Lys Arg Ala Ala  
 675 680 685  
 Glu Asp Val Leu Glu Gly Met Asp Ser Thr Leu Thr Gln Glu Glu Ala  
 690 695 700  
 Gly Val Ala Glu Arg Leu Ala Met His Ile Ala Asp Asn Val Asp Thr  
 705 710 715 720  
 Asp Asp Phe Gln Thr Lys Asn Asp Ser Ile Ser Cys Lys Leu Ser Phe  
 725 730 735  
 Ile Met Ser Leu Leu Glu Asn Leu Ile Pro Glu Gly His Arg Val Leu  
 740 745 750  
 Ile Phe Ser Gln Thr Arg Lys Met Leu Asn Leu Ile Gln Asp Ser Leu  
 755 760 765  
 Thr Ser Asn Gly Tyr Ser Phe Leu Arg Ile Asp Gly Thr Thr Lys Ala  
 770 775 780  
 Pro Asp Arg Leu Lys Thr Val Glu Glu Phe Gln Glu Gly His Val Ala  
 785 790 795 800  
 Pro Ile Phe Leu Leu Thr Ser Gln Val Gly Gly Leu Gly Leu Thr Leu  
 805 810 815  
 Thr Lys Ala Asp Arg Val Ile Val Val Asp Pro Ala Trp Asn Pro Ser  
 820 825 830  
 Thr Asp Asn Gln Ser Val Asp Arg Ala Tyr Arg Ile Gly Gln Thr Lys  
 835 840 845  
 Asp Val Ile Val Tyr Arg Leu Met Thr Ser Ala Thr Val Glu Glu Lys  
 850 855 860  
 Ile Tyr Arg Lys Gln Val Tyr Lys Gly Gly Leu Phe Lys Thr Ala Thr  
 865 870 875 880  
 Glu His Lys Glu Gln Ile Arg Tyr Phe Ser Gln Gln Asp Leu Arg Glu  
 885 890 895  
 Leu Phe Ser Leu Pro Lys Gly Gly Phe Asp Val Ser Pro Thr Gln Gln  
 900 905 910  
 Gln Leu Tyr Glu Glu His Tyr Asn Gln Ile Lys Leu Asp Glu Lys Leu  
 915 920 925  
 Glu Ser His Val Lys Phe Leu Glu Thr Leu Gly Ile Ala Gly Val Ser  
 930 935 940  
 His His Ser Leu Leu Phe Ser Lys Thr Ala Pro Ile Gln Ala Ile Gln  
 945 950 955 960  
 Lys Asp Glu Glu Glu Gln Ile Arg Arg Glu Thr Ala Leu Leu Leu Gly  
 965 970 975  
 Arg Ala Ser Ala Ser Ile Ser Gln Asp Thr Val Ile Asn Gly Ala Asp  
 980 985 990  
 Tyr Ala Phe Lys Pro Lys Asp Val Asn Leu Asp Lys Arg Ile Asn Ile  
 995 1000 1005  
 Ser Pro Val Asp Asp Lys Glu Leu Ser Glu Ser Val Ile Lys Ala  
 1010 1015 1020  
 Arg Leu Asn Arg Leu Thr Met Leu Leu Gln Asn Lys Gly Thr Val  
 1025 1030 1035  
 Ser Arg Leu Pro Asp Gly Gly Ala Lys Ile Gln Lys Gln Ile Ala

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**61****62**

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1040 1045 1050

Glu Leu Thr Arg Glu Leu Lys Asp Met Lys Ala Ala Glu Arg Ile  
 1055 1060 1065

Asn Met Pro Gln Val Ile Asp Leu Glu Glu Asp Ile Ser Arg Lys  
 1070 1075 1080

Met Gln Lys Gly Leu Asn Leu  
 1085 1090

&lt;210&gt; SEQ ID NO 21

&lt;211&gt; LENGTH: 406

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: MISC\_FEATURE

&lt;223&gt; OTHER INFORMATION: At5G47440

&lt;400&gt; SEQUENCE: 21

Met Glu Gly Gly Phe Tyr Ser Asp Trp Asn Asp Ser Ser Ser Ser Leu  
 1 5 10 15

Phe Gly Ser Glu Asn Pro Glu His Glu Leu Glu Glu Gly Asn Val Arg  
 20 25 30

Ser Glu Glu Ile Val Ser Gln Ile Pro Gln Pro Gln Thr Pro Arg Glu  
 35 40 45

Pro Met Lys Phe Leu Ser Arg Ser Trp Ser Leu Ser Ala Ser Glu Ile  
 50 55 60

Ser Lys Ala Leu Ala Gln Lys Gln Arg Gln Gln Arg Asp Leu Phe Ser  
 65 70 75 80

Val Ser Gln Asn Ser Pro Arg Gly Phe Phe Gln Asp Val Ala Ala Asp  
 85 90 95

Pro Leu Met Ala Glu Asn Ile Met Asn Ser Ala Gly Thr Arg Arg Ser  
 100 105 110

Gly Arg Leu Ser Lys Trp Phe His His Lys Gln His Thr Asn Pro Ser  
 115 120 125

Thr Met Arg Ile Pro Arg Lys Lys Asp Lys Ala Arg Val Gln Lys Ala  
 130 135 140

His Val His Ser Ala Val Ser Ile Ala Ala Leu Ala Ala Gly Leu Ala  
 145 150 155 160

Ser Val Thr Ser Glu Glu Ser Cys Ser Lys Glu Ser Cys Ser Met Met  
 165 170 175

Ala Leu Ala Leu Ala Ser Ala Thr Glu Leu Leu Ala Ser His Cys Ile  
 180 185 190

Asp Met Ala Glu Gln Ala Gly Ala Asp His Thr Cys Val Ala Ser Thr  
 195 200 205

Val Arg Ser Ser Val Asp Ile His Ser Pro Gly Asp Leu Met Thr Leu  
 210 215 220

Thr Ala Ala Ala Ala Thr Ala Leu Arg Gly Glu Ala Ala Leu Lys Val  
 225 230 235 240

Arg Gln Pro Lys Glu Ser Arg Lys Asn Ala Thr Ile Thr Pro Cys Glu  
 245 250 255

Arg Ser Phe Ser Asp Ser His Trp Pro Gly Glu Asn Cys Gln Phe Arg  
 260 265 270

Leu Glu Glu Pro Asn Leu Pro Leu Glu Gly Glu Leu Val Gln Cys Ala  
 275 280 285

Arg Asn Gly Leu Gln Arg Asn Lys Arg Val Cys Val Tyr Ile Asn Lys  
 290 295 300

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Lys Ser Gln Val Met Ile Lys Leu Lys Ser Lys His Val Gly Gly Ala  
305 310 315 320

Phe Ser Lys Lys Ile Lys Cys Val Val Tyr Gly Val Cys Asp Glu Ile  
325 330 335

Ser Ala Trp Pro Cys Arg Lys Glu Arg Glu Asn Ser Glu Glu Val Tyr  
340 345 350

Phe Gly Leu Lys Thr Gly Gln Gly Leu Leu Glu Phe Lys Cys Lys Ser  
355 360 365

Lys Ile Gln Lys Gln Arg Trp Val Ala Gly Ile Gln Ser Asn Leu Arg  
370 375 380

Leu Val Ser Cys Leu Glu Ala Ala Lys Cys Ser Leu Glu Ser Leu Ser  
385 390 395 400

Leu Ser Asn Arg Met Arg  
405

<210> SEQ\_ID NO 22  
<211> LENGTH: 250  
<212> TYPE: PRT  
<213> ORGANISM: Arabidopsis thaliana  
<220> FEATURE:  
<221> NAME/KEY: MISC\_FEATURE  
<223> OTHER INFORMATION: At1G69530

<400> SEQUENCE: 22

Met Ala Leu Val Thr Phe Leu Phe Ile Ala Thr Leu Gly Ala Met Thr  
1 5 10 15

Ser His Val Asn Gly Tyr Ala Gly Gly Trp Val Asn Ala His Ala  
20 25 30

Thr Phe Tyr Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala Cys  
35 40 45

Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala Ala  
50 55 60

Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe  
65 70 75 80

Glu Ile Arg Cys Gln Asn Asp Gly Lys Trp Cys Leu Pro Gly Ser Ile  
85 90 95

Val Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn  
100 105 110

Asn Ala Gly Gly Trp Cys Asn Pro Pro Gln Gln His Phe Asp Leu Ser  
115 120 125

Gln Pro Val Phe Gln Arg Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro  
130 135 140

Val Ala Tyr Arg Arg Val Pro Cys Val Arg Arg Gly Gly Ile Arg Phe  
145 150 155 160

Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val  
165 170 175

Gly Gly Ala Gly Asp Val His Ser Ala Met Val Lys Gly Ser Arg Thr  
180 185 190

Gly Trp Gln Ala Met Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn  
195 200 205

Ser Tyr Leu Asn Gly Gln Ser Leu Ser Phe Lys Val Thr Thr Ser Asp  
210 215 220

Gly Gln Thr Ile Val Ser Asn Asn Val Ala Asn Ala Gly Trp Ser Phe  
225 230 235 240

Gly Gln Thr Phe Thr Gly Ala Gln Leu Arg  
245 250

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<210> SEQ\_ID NO 23  
 <211> LENGTH: 365  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At4G32460  
  
 <400> SEQUENCE: 23

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Glu | Met | Gly | Val | Ile | Val | Leu | Leu | Leu | His | Ser | Phe | Phe |     |
| 1   |     |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Tyr | Val | Ala | Phe | Cys | Phe | Asn | Asp | Gly | Leu | Leu | Pro | Asn | Gly | Asp | Phe |
|     | 20  |     |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Leu | Gly | Pro | Arg | His | Ser | Asp | Met | Lys | Gly | Thr | Gln | Val | Ile | Asn |
|     | 35  |     |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ile | Thr | Ala | Ile | Pro | Asn | Trp | Glu | Leu | Ser | Gly | Phe | Val | Glu | Tyr | Ile |
|     | 50  |     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Pro | Ser | Gly | His | Lys | Gln | Gly | Asp | Met | Ile | Leu | Val | Val | Pro | Lys | Gly |
|     | 65  |     |     |     |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Ala | Phe | Ala | Val | Arg | Leu | Gly | Asn | Glu | Ala | Ser | Ile | Lys | Gln | Lys | Ile |
|     | 85  |     |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Val | Lys | Lys | Gly | Ser | Tyr | Tyr | Ser | Ile | Thr | Phe | Ser | Ala | Ala | Arg |
|     | 100 |     |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Cys | Ala | Gln | Asp | Glu | Arg | Leu | Asn | Val | Ser | Val | Ala | Pro | His | His |
|     | 115 |     |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Ala | Val | Met | Pro | Ile | Gln | Thr | Val | Tyr | Ser | Ser | Gly | Trp | Asp | Leu |     |
|     | 130 |     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |
| Tyr | Ser | Trp | Ala | Phe | Lys | Ala | Gln | Ser | Asp | Tyr | Ala | Asp | Ile | Val | Ile |
|     | 145 |     |     |     |     |     |     | 150 |     |     |     |     | 155 |     | 160 |
| His | Asn | Pro | Gly | Val | Glu | Glu | Asp | Pro | Ala | Cys | Gly | Pro | Leu | Ile | Asp |
|     | 165 |     |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gly | Val | Ala | Met | Arg | Ala | Leu | Phe | Pro | Pro | Arg | Pro | Thr | Asn | Lys | Asn |
|     | 180 |     |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Leu | Lys | Asn | Gly | Gly | Phe | Glu | Glu | Gly | Pro | Trp | Val | Leu | Pro | Asn |
|     | 195 |     |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Ile | Ser | Ser | Gly | Val | Leu | Ile | Pro | Pro | Asn | Ser | Ile | Asp | Asp | His | Ser |
|     | 210 |     |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |
| Pro | Leu | Pro | Gly | Trp | Met | Val | Glu | Ser | Leu | Lys | Ala | Val | Lys | Tyr | Ile |
|     | 225 |     |     |     |     |     |     | 230 |     |     |     |     | 235 |     | 240 |
| Asp | Ser | Asp | His | Phe | Ser | Val | Pro | Gln | Gly | Arg | Arg | Ala | Val | Glu | Leu |
|     | 245 |     |     |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Val | Ala | Gly | Lys | Glu | Ser | Ala | Val | Ala | Gln | Val | Val | Arg | Thr | Ile | Pro |
|     | 260 |     |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Lys | Thr | Tyr | Val | Leu | Ser | Phe | Ser | Val | Gly | Asp | Ala | Ser | Asn | Ala |
|     | 275 |     |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Cys | Ala | Gly | Ser | Met | Ile | Val | Glu | Ala | Phe | Ala | Gly | Lys | Asp | Thr | Ile |
|     | 290 |     |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |
| Lys | Val | Pro | Tyr | Glu | Ser | Lys | Gly | Lys | Gly | Gly | Phe | Lys | Arg | Ser | Ser |
|     | 305 |     |     |     |     |     |     | 310 |     |     |     |     | 315 |     | 320 |
| Leu | Arg | Phe | Val | Ala | Val | Ser | Ser | Arg | Thr | Arg | Val | Met | Phe | Tyr | Ser |
|     | 325 |     |     |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Thr | Phe | Tyr | Ala | Met | Arg | Asn | Asp | Asp | Phe | Ser | Ser | Leu | Cys | Gly | Pro |
|     | 340 |     |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Ile | Asp | Asp | Val | Lys | Leu | Leu | Ser | Ala | Arg | Arg | Pro |     |     |     |

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355                    360                    365

<210> SEQ ID NO 24  
 <211> LENGTH: 129  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At5G67070

<400> SEQUENCE: 24

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ser | Ser | Leu | Asn | Leu | Leu | Ile | Leu | Ser | Leu | Leu | Thr |     |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ile | Ser | Leu | Gln | Arg | Ser | Glu | Ser | Leu | Ser | Asp | Asn | Pro | Ser | Leu |
|     |     |     |     |     | 20  |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Leu | Leu | Pro | Asp | Gly | Phe | Asp | Trp | Pro | Ile | Ser | His | Ser | Asp | Glu |
|     |     |     |     |     | 35  |     |     | 40  |     |     | 45  |     |     |     |     |
| Phe | Asp | Ile | Ile | Asp | Gly | Glu | Glu | Ser | Phe | Glu | Val | Thr | Glu | Glu | Asp |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Asp | Gly | Val | Thr | Asp | Arg | Arg | Ser | Leu | Tyr | Trp | Arg | Arg | Thr | Lys | Tyr |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Tyr | Ile | Ser | Tyr | Gly | Ala | Leu | Ser | Ala | Asn | Arg | Val | Pro | Cys | Pro | Pro |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |
| Arg | Ser | Gly | Arg | Ser | Tyr | Tyr | Thr | His | Asn | Cys | Phe | Arg | Ala | Arg | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Val | His | Pro | Tyr | Ser | Arg | Gly | Cys | Ser | Ser | Ile | Thr | Arg | Cys | Arg |
|     |     |     |     |     | 115 |     |     | 120 |     |     |     | 125 |     |     |     |

<210> SEQ ID NO 25  
<211> LENGTH: 418  
<212> TYPE: PRT  
<213> ORGANISM: Arabidopsis thaliana  
<220> FEATURE:  
<221> NAME/KEY: MISC\_FEATURE  
<223> OTHER INFORMATION: At4G13210

<400> SEQUENCE: 25

Met Val Val Ala Arg Thr Leu Phe Ser Ile Ser Ala Thr Leu Ile Ile  
1 5 10 15

Phe Leu Ala Leu Phe Leu His Val Asn Ala Leu Ser Asp Gly Glu Trp  
20 25 30

His Glu His Ala Val Lys Asp Pro Glu Glu Ile Ala Ala Met Val Asp  
35 40 45

Met Ser Ile Arg Asn Ser Thr Tyr Arg Arg Lys Leu Gly Phe Phe Ser  
50 55 60

Ser Cys Ser Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Lys  
65 70 75 80

Lys Trp His Arg Arg Lys Arg Leu Ala Asp Cys Ala Ile Gly Phe  
85 90 95

Gly Arg Asn Ala Val Gly Gly Arg Asp Gly Arg Tyr Tyr Ile Val Thr  
100 105 110

Asp Pro Ser Asp His Asp Pro Val Thr Pro Lys Pro Gly Thr Leu Arg  
115 120 125

Tyr Ala Val Ile Gln Asp Glu Pro Leu Trp Ile Val Phe Lys Arg Asp  
130 135 140

Met Val Ile Thr Leu Ser Gln Glu Leu Ile Met Asn Ser Phe Lys Thr  
145 150 155 160

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Ile Asp Gly Arg Gly Val Asn Val His Ile Ala Gly Gly Ala Cys Leu  
165 170 175

Thr Val Gln Tyr Val Thr Asn Ile Ile His Gly Ile Asn Ile His  
180 185 190

Asp Cys Lys Arg Thr Gly Asn Ala Met Val Arg Ser Ser Glu Ser His  
195 200 205

Tyr Gly Trp Arg Thr Met Ala Asp Gly Asp Gly Ile Ser Ile Phe Gly  
210 215 220

Ser Ser His Ile Trp Ile Asp His Asn Ser Leu Ser Ser Cys Ala Asp  
225 230 235 240

Gly Leu Ile Asp Ala Ile Met Gly Ser Thr Ala Ile Thr Ile Ser Asn  
245 250 255

Asn Tyr Leu Thr His His Asn Glu Ala Ile Leu Leu Gly His Thr Asp  
260 265 270

Ser Tyr Thr Arg Asp Lys Met Met Gln Val Thr Ile Ala Tyr Asn His  
275 280 285

Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr  
290 295 300

Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile  
305 310 315 320

Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Phe Leu  
325 330 335

Ala Pro Gly Asn Arg Phe Ala Lys Glu Val Thr Lys Arg Val Gly Ala  
340 345 350

Gly Lys Gly Glu Trp Asn Asn Trp Asn Trp Arg Ser Gln Gly Asp Leu  
355 360 365

Met Leu Asn Gly Ala Tyr Phe Thr Ser Ser Gly Ala Gly Ala Ser Ala  
370 375 380

Asn Tyr Ala Arg Ala Ser Ser Leu Ala Ala Lys Ser Ser Ser Leu Val  
385 390 395 400

Gly Met Leu Thr Ser Ser Ser Gly Ala Leu Lys Cys Arg Ile Gly Thr  
405 410 415

Leu Cys

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<210> SEQ ID NO 26
<211> LENGTH: 461
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: At1G80370

<400> SEQUENCE: 26

Met Gly Lys Glu Asn Ala Val Ser Gly Asn Ser Ile Pro Ile His Gly
1 5 10 15

Arg Pro Val Thr Arg Ala Leu Ala Ser Ala Leu Arg Ala Ser Ser Lys
20 25 30

Leu Ile Thr Ser Ser Glu Val Ala Ala Thr Thr Gln Asn Gln Gly Arg
35 40 45

Val Leu Arg Ala Lys Ser Lys Arg Thr Ala Leu Asp Glu Lys Lys Ala
50 55 60

Asn Ala Pro Lys Lys Arg Ala Val Leu Lys Asp Ile Thr Asn Val Thr
65 70 75 80

Cys Glu Asn Ser Tyr Thr Ser Cys Phe Ser Val Ala Val Glu Asn Ile
85 90 95

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Lys Gln Ile Lys Lys Gly Arg Gln Ser Ser Ser Ser Lys Val Ala  
100 105 110

Ser Ser Ser Ala Thr Ser Gln Val Thr Asp Ala Lys Val Glu Val Val  
115 120 125

Ser Asn Ser Ala Gly Ala Ser Leu Ser Val Phe Thr Asp Thr Ser Leu  
130 135 140

Gly Thr Asn Glu Thr Ser Tyr Ser Ile Ile Ala Lys Pro Ser Ser Arg  
145 150 155 160

Ser Pro Pro Arg Pro Phe Gly Thr Val Glu Arg Ser Cys Gly Ala  
165 170 175

Ser Ser Pro Lys Phe Val Asp Ile Asp Ser Asp Asp Lys Asp Pro Leu  
180 185 190

Leu Cys Ser Leu Tyr Ala Pro Asp Ile Tyr Tyr Asn Leu Arg Val Ala  
195 200 205

Glu Leu Lys Arg Arg Pro Phe Pro Asp Phe Met Glu Lys Thr Gln Arg  
210 215 220

Asp Val Thr Glu Thr Met Arg Gly Ile Leu Val Asp Trp Leu Val Glu  
225 230 235 240

Val Ser Glu Glu Tyr Thr Leu Val Pro Asp Thr Leu Tyr Leu Thr Val  
245 250 255

Tyr Leu Ile Asp Trp Phe Leu His Gly Asn Tyr Val Glu Arg Gln Arg  
260 265 270

Leu Gln Leu Leu Gly Ile Thr Cys Met Leu Ile Ala Ser Lys Tyr Glu  
275 280 285

Glu Ile His Ala Pro Arg Ile Glu Glu Phe Cys Phe Ile Thr Asp Asn  
290 295 300

Thr Tyr Thr Arg Asp Gln Val Leu Glu Met Glu Ser Gln Val Leu Lys  
305 310 315 320

His Phe Ser Phe Gln Ile Tyr Thr Pro Thr Ser Lys Thr Phe Leu Arg  
325 330 335

Arg Phe Leu Arg Ala Ala Gln Val Ser Phe Pro Asn Gln Ser Leu Glu  
340 345 350

Met Glu Phe Leu Ala Asn Tyr Leu Thr Glu Leu Thr Leu Met Asp Tyr  
355 360 365

Pro Phe Leu Lys Phe Leu Pro Ser Ile Ile Ala Ala Ser Ala Val Phe  
370 375 380

Leu Ala Lys Trp Thr Leu Asn Gln Ser Ser His Pro Trp Asn Pro Thr  
385 390 395 400

Leu Glu His Tyr Thr Tyr Lys Ala Ser Asp Leu Lys Ala Ser Val  
405 410 415

His Ala Leu Gln Asp Leu Gln Leu Asn Thr Lys Gly Cys Ser Leu Asn  
420 425 430

Ser Ile Arg Met Lys Tyr Arg Gln Asp Lys Phe Lys Ser Val Ala Val  
435 440 445

Phe Ser Ser Gly Glu Leu Pro Asp Lys Leu Phe Ile Ser  
450 455 460

<210> SEQ\_ID NO 27  
<211> LENGTH: 167  
<212> TYPE: PRT  
<213> ORGANISM: Arabidopsis thaliana  
<220> FEATURE:  
<221> NAME/KEY: MISC\_FEATURE  
<223> OTHER INFORMATION: At3G01070

-continued

&lt;400&gt; SEQUENCE: 27

Met Ala Arg Val Ala Val Leu Val Ala Gly Ala Val Leu Ala Phe Leu  
 1               5               10               15

Leu Ala Ala Thr Asn Val Thr Ala Lys Arg Trp Thr Val Gly Asp Asn  
 20              25              30

Lys Phe Trp Asn Pro Asn Ile Asn Tyr Thr Ile Trp Ala Gln Asp Lys  
 35              40              45

His Phe Tyr Leu Asp Asp Trp Leu Tyr Phe Val Tyr Glu Arg Asn Gln  
 50              55              60

Tyr Asn Val Ile Glu Val Asn Glu Thr Asn Tyr Ile Ser Cys Asn Pro  
 65              70              75              80

Asn Asn Pro Ile Ala Asn Trp Ser Arg Gly Ala Gly Arg Asp Leu Val  
 85              90              95

His Leu Asn Val Thr Arg His Tyr Tyr Leu Ile Ser Gly Asn Gly Gly  
 100             105             110

Gly Cys Tyr Gly Gly Met Lys Leu Ala Val Leu Val Glu Lys Pro Pro  
 115             120             125

Pro Pro Pro Ala Ala Ala Pro Asn Lys Asn Ser Ala Arg Arg Thr Phe  
 130             135             140

Ser Val Ser Gly Phe Ala Tyr Gln Phe Leu Ile Pro Val Ala Val Phe  
 145             150             155             160

Ala Ala Val Gly Thr Arg Tyr  
 165

&lt;210&gt; SEQ\_ID NO 28

&lt;211&gt; LENGTH: 390

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: MISC\_FEATURE

&lt;223&gt; OTHER INFORMATION: At1G61580

&lt;400&gt; SEQUENCE: 28

Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe  
 1               5               10               15

Leu Pro Arg Lys Arg Ala Ser Arg His Arg Gly Lys Val Lys Ala Phe  
 20              25              30

Pro Lys Asp Asp Pro Thr Lys Pro Cys Arg Leu Thr Ser Phe Leu Gly  
 35              40              45

Tyr Lys Ala Gly Met Thr His Ile Val Arg Asp Val Glu Lys Pro Gly  
 50              55              60

Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu  
 65              70              75              80

Thr Pro Pro Met Val Val Val Gly Val Val Gly Tyr Val Lys Thr Pro  
 85              90              95

Arg Gly Leu Arg Ser Leu Cys Thr Val Trp Ala Gln His Leu Ser Glu  
 100             105             110

Glu Leu Arg Arg Arg Phe Tyr Lys Asn Trp Ala Lys Ser Lys Lys  
 115             120             125

Ala Phe Thr Arg Tyr Ser Lys Lys His Glu Thr Glu Glu Gly Lys Lys  
 130             135             140

Asp Ile Gln Ser Gln Leu Glu Lys Met Lys Lys Tyr Cys Ser Val Ile  
 145             150             155             160

Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln  
 165             170             175

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Lys Lys Ala His Leu Asn Glu Ile Gln Ile Asn Gly Gly Asp Ile Ala  
180 185 190

Lys Lys Val Asp Tyr Ala Cys Ser Leu Phe Glu Lys Gln Val Pro Val  
195 200 205

Asp Ala Ile Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr  
210 215 220

Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg  
225 230 235 240

Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly  
245 250 255

Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln  
260 265 270

Asn Gly Tyr His His Arg Thr Glu Met Asn Lys Lys Val Tyr Arg Val  
275 280 285

Gly Lys Val Gly Gln Glu Thr His Ser Ala Met Thr Glu Tyr Asp Arg  
290 295 300

Thr Glu Lys Asp Ile Thr Pro Met Gly Gly Phe Pro His Tyr Gly Ile  
305 310 315 320

Val Lys Glu Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys  
325 330 335

Lys Arg Val Val Thr Leu Arg Gln Thr Leu Leu Lys Gln Thr Ser Arg  
340 345 350

Leu Ala Met Glu Glu Ile Lys Leu Lys Phe Ile Asp Ala Ala Ser Asn  
355 360 365

Gly Gly His Gly Arg Phe Gln Thr Ser Gln Glu Lys Ala Lys Phe Tyr  
370 375 380

Gly Arg Thr Ile Lys Ala  
385 390

<210> SEQ\_ID NO 29  
<211> LENGTH: 175  
<212> TYPE: PRT  
<213> ORGANISM: Arabidopsis thaliana  
<220> FEATURE:  
<221> NAME/KEY: MISC\_FEATURE  
<223> OTHER INFORMATION: At2G46990

<400> SEQUENCE: 29

Met Gly Arg Gly Arg Ser Ser Ser Ser Ser Ser Ile Glu Ser Ser Ser  
1 5 10 15

Lys Ser Asn Pro Phe Gly Ala Ser Ser Ser Thr Arg Asn Leu Ser Thr  
20 25 30

Asp Leu Arg Leu Gly Leu Ser Phe Gly Thr Ser Ser Gly Thr Gln Tyr  
35 40 45

Phe Asn Gly Gly Tyr Gly Tyr Ser Val Ala Ala Pro Ala Val Glu Asp  
50 55 60

Ala Glu Tyr Val Ala Ala Val Glu Glu Glu Glu Asn Glu Cys Asn  
65 70 75 80

Ser Val Gly Ser Phe Tyr Val Lys Val Asn Met Glu Gly Val Pro Ile  
85 90 95

Gly Arg Lys Ile Asp Leu Met Ser Leu Asn Gly Tyr Arg Asp Leu Ile  
100 105 110

Arg Thr Leu Asp Phe Met Phe Asn Ala Ser Ile Leu Trp Ala Glu Glu  
115 120 125

Glu Asp Met Cys Asn Glu Lys Ser His Val Leu Thr Tyr Ala Asp Lys  
130 135 140

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Glu Gly Asp Trp Met Met Val Gly Asp Val Pro Trp Glu Met Phe Leu  
 145                   150                   155                   160

Ser Thr Val Arg Arg Leu Lys Ile Ser Arg Ala Asn Tyr His Tyr  
 165                   170                   175

<210> SEQ ID NO 30

<211> LENGTH: 716

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: MISC\_FEATURE

<223> OTHER INFORMATION: At4G02060

<400> SEQUENCE: 30

Met Lys Asp His Asp Phe Asp Gly Asp Lys Gly Leu Ala Lys Gly Phe  
 1                   5                   10                   15

Leu Glu Asn Phe Ala Asp Ala Asn Gly Arg Ser Lys Tyr Met Glu Ile  
 20                   25                   30

Leu Gln Glu Val Ser Asn Arg Lys Ile Arg Ala Ile Gln Val Asp Leu  
 35                   40                   45

Asp Asp Leu Phe Asn Tyr Lys Asp Glu Ser Glu Glu Phe Leu Gly Arg  
 50                   55                   60

Leu Thr Glu Asn Thr Arg Arg Tyr Val Ser Ile Phe Ser Ala Ala Val  
 65                   70                   75                   80

Asp Glu Leu Leu Pro Glu Pro Thr Glu Ala Phe Pro Asp Asp Asp His  
 85                   90                   95

Asp Ile Leu Met Thr Gln Arg Ala Asp Asp Gly Thr Asp Asn Pro Asp  
 100                 105                 110

Val Ser Asp Pro His Gln Gln Ile Pro Ser Glu Ile Lys Arg Tyr Tyr  
 115                 120                 125

Glu Val Tyr Phe Lys Ala Pro Ser Lys Gly Arg Pro Ser Thr Ile Arg  
 130                 135                 140

Glu Val Lys Ala Ser His Ile Gly Gln Leu Val Arg Ile Ser Gly Ile  
 145                 150                 155                 160

Val Thr Arg Cys Ser Asp Val Lys Pro Leu Met Ala Val Ala Val Tyr  
 165                 170                 175

Thr Cys Glu Asp Cys Gly His Glu Ile Tyr Gln Glu Val Thr Ser Arg  
 180                 185                 190

Val Phe Met Pro Leu Phe Lys Cys Pro Ser Ser Arg Cys Arg Leu Asn  
 195                 200                 205

Ser Lys Ala Gly Asn Pro Ile Leu Gln Leu Arg Ala Ser Lys Phe Leu  
 210                 215                 220

Lys Phe Gln Glu Ala Lys Met Gln Glu Leu Ala Glu His Val Pro Lys  
 225                 230                 235                 240

Gly His Ile Pro Arg Ser Met Thr Val His Leu Arg Gly Glu Leu Thr  
 245                 250                 255

Arg Lys Val Ser Pro Gly Asp Val Val Glu Phe Ser Gly Ile Phe Leu  
 260                 265                 270

Pro Ile Pro Tyr Thr Gly Phe Lys Ala Leu Arg Ala Gly Leu Val Ala  
 275                 280                 285

Asp Thr Tyr Leu Glu Ala Thr Ser Val Thr His Phe Lys Lys Tyr  
 290                 295                 300

Glu Glu Tyr Glu Phe Gln Lys Asp Glu Glu Gln Ile Ala Arg Leu  
 305                 310                 315                 320

Ala Glu Asp Gly Asp Ile Tyr Asn Lys Leu Ser Arg Ser Leu Ala Pro

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| 325   | 330 | 335 |
|---|-----|-----|
| Glu Ile Tyr Gly His Glu Asp Ile Lys Lys Ala Leu Leu Leu Leu     |     |     |
| 340   | 345 | 350 |
| Val Gly Ala Pro His Arg Gln Leu Lys Asp Gly Met Lys Ile Arg Gly |     |     |
| 355   | 360 | 365 |
| Asp Val His Ile Cys Leu Met Gly Asp Pro Gly Val Ala Lys Ser Gln |     |     |
| 370   | 375 | 380 |
| Leu Leu Lys His Ile Ile Asn Val Ala Pro Arg Gly Val Tyr Thr Thr |     |     |
| 385   | 390 | 395 |
| Gly Lys Gly Ser Ser Gly Val Gly Leu Thr Ala Ala Val Met Arg Asp |     |     |
| 405   | 410 | 415 |
| Gln Val Thr Asn Glu Met Val Leu Glu Gly Gly Ala Leu Val Leu Ala |     |     |
| 420   | 425 | 430 |
| Asp Met Gly Ile Cys Ala Ile Asp Glu Phe Asp Lys Met Asp Glu Ser |     |     |
| 435   | 440 | 445 |
| Asp Arg Thr Ala Ile His Glu Val Met Glu Gln Gln Thr Val Ser Ile |     |     |
| 450   | 455 | 460 |
| Ala Lys Ala Gly Ile Thr Thr Ser Leu Asn Ala Arg Thr Ala Val Leu |     |     |
| 465   | 470 | 475 |
| Ala Ala Ala Asn Pro Ala Trp Gly Arg Tyr Asp Leu Arg Arg Thr Pro |     |     |
| 485   | 490 | 495 |
| Ala Glu Asn Ile Asn Leu Pro Pro Ala Leu Leu Ser Arg Phe Asp Leu |     |     |
| 500   | 505 | 510 |
| Leu Trp Leu Ile Leu Asp Arg Ala Asp Met Asp Ser Asp Leu Glu Leu |     |     |
| 515   | 520 | 525 |
| Ala Lys His Val Leu His Val His Gln Thr Glu Glu Ser Pro Ala Leu |     |     |
| 530   | 535 | 540 |
| Gly Phe Glu Pro Leu Glu Pro Asn Ile Leu Arg Ala Tyr Ile Ser Ala |     |     |
| 545   | 550 | 555 |
| Ala Arg Arg Leu Ser Pro Tyr Val Pro Ala Glu Leu Glu Tyr Ile     |     |     |
| 565   | 570 | 575 |
| Ala Thr Ala Tyr Ser Ser Ile Arg Gln Glu Glu Ala Lys Ser Asn Thr |     |     |
| 580   | 585 | 590 |
| Pro His Ser Tyr Thr Thr Val Arg Thr Leu Leu Ser Ile Leu Arg Ile |     |     |
| 595   | 600 | 605 |
| Ser Ala Ala Leu Ala Arg Leu Arg Phe Ser Glu Ser Val Ala Gln Ser |     |     |
| 610   | 615 | 620 |
| Asp Val Asp Glu Ala Leu Arg Leu Met Gln Met Ser Lys Ile Ser Leu |     |     |
| 625   | 630 | 635 |
| Tyr Ala Asp Asp Arg Gln Lys Ala Gly Leu Asp Ala Ile Ser Asp Thr |     |     |
| 645   | 650 | 655 |
| Tyr Ser Ile Ile Arg Asp Glu Ala Ala Arg Ser Lys Lys Thr His Val |     |     |
| 660   | 665 | 670 |
| Ser Tyr Ala Asn Ala Leu Asn Trp Ile Ser Arg Lys Gly Tyr Ser Glu |     |     |
| 675   | 680 | 685 |
| Ala Gln Leu Lys Glu Cys Leu Glu Glu Tyr Ala Ala Leu Asn Val Trp |     |     |
| 690   | 695 | 700 |
| Gln Ile Asp Pro His Thr Phe Asp Ile Arg Phe Ile                 |     |     |
| 705   | 710 | 715 |

<210> SEQ ID NO 31  
<211> LENGTH: 351  
<212> TYPE: PRT  
<213> ORGANISM: Arabidopsis thaliana

-continued

<220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At2G33620

<400> SEQUENCE: 31

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Met Ser Gly Ser Glu Thr Gly Leu Met Ala Ala Thr Arg Glu Ser Met
 1           5          10          15

Gln Phe Thr Met Ala Leu His Gln Gln Gln His Ser Gln Ala Gln
 20          25          30

Pro Gln Gln Ser Gln Asn Arg Pro Leu Ser Phe Gly Gly Asp Asp Gly
 35          40          45

Thr Ala Leu Tyr Lys Gln Pro Met Arg Ser Val Ser Pro Pro Gln Gln
 50          55          60

Tyr Gln Pro Asn Ser Ala Gly Glu Asn Ser Val Leu Asn Met Asn Leu
 65          70          75          80

Pro Gly Gly Glu Ser Gly Gly Met Thr Gly Thr Gly Ser Glu Pro Val
 85          90          95

Lys Lys Arg Arg Gly Arg Pro Arg Lys Tyr Gly Pro Asp Ser Gly Glu
100          105         110

Met Ser Leu Gly Leu Asn Pro Gly Ala Pro Ser Phe Thr Val Ser Gln
115          120         125

Pro Ser Ser Gly Gly Asp Gly Glu Lys Lys Arg Gly Arg Pro Pro
130          135         140

Gly Ser Ser Ser Lys Arg Leu Lys Leu Gln Ala Leu Gly Ser Thr Gly
145          150         155         160

Ile Gly Phe Thr Pro His Val Leu Thr Val Leu Ala Gly Glu Asp Val
165          170         175

Ser Ser Lys Ile Met Ala Leu Thr His Asn Gly Pro Arg Ala Val Cys
180          185         190

Val Leu Ser Ala Asn Gly Ala Ile Ser Asn Val Thr Leu Arg Gln Ser
195          200         205

Ala Thr Ser Gly Gly Thr Val Thr Tyr Glu Gly Arg Phe Glu Ile Leu
210          215         220

Ser Leu Ser Gly Ser Phe His Leu Leu Glu Asn Asn Gly Gln Arg Ser
225          230         235         240

Arg Thr Gly Leu Ser Val Ser Leu Ser Ser Pro Asp Gly Asn Val
245          250         255

Leu Gly Gly Ser Val Ala Gly Leu Leu Ile Ala Ala Ser Pro Val Gln
260          265         270

Ile Val Val Gly Ser Phe Leu Pro Asp Gly Glu Lys Glu Pro Lys Gln
275          280         285

His Val Gly Gln Met Gly Leu Ser Ser Pro Val Leu Pro Arg Val Ala
290          295         300

Pro Thr Gln Val Leu Met Thr Pro Ser Ser Pro Gln Ser Arg Gly Thr
305          310         315         320

Met Ser Glu Ser Ser Cys Gly Gly His Gly Ser Pro Ile His Gln
325          330         335

Ser Thr Gly Gly Pro Tyr Asn Asn Thr Ile Asn Met Pro Trp Lys
340          345         350

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<210> SEQ ID NO 32  
 <211> LENGTH: 1492  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE

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&lt;223&gt; OTHER INFORMATION: At5G67100

&lt;400&gt; SEQUENCE: 32

Met Ser Gly Asp Asn Ser Thr Glu Thr Gly Arg Arg Arg Ser Arg Gly  
 1 5 10 15

Ala Glu Ala Ser Ser Arg Lys Asp Thr Leu Glu Arg Leu Lys Ala Ile  
 20 25 30

Arg Gln Gly Gly Ile Arg Ser Ala Ser Gly Gly Tyr Asp Ile Arg  
 35 40 45

Leu Gln Lys Pro Ile Phe Asp Thr Val Asp Asp Glu Glu Tyr Asp Ala  
 50 55 60

Leu Val Ser Arg Arg Arg Glu Glu Ala Arg Gly Phe Val Val Glu Asp  
 65 70 75 80

Gly Glu Gly Asp Leu Gly Tyr Leu Asp Glu Gly Glu Glu Asp  
 85 90 95

Trp Ser Lys Pro Ser Gly Pro Glu Ser Thr Asp Glu Ser Asp Asp Gly  
 100 105 110

Gly Arg Phe Ser Gly Arg Leu Lys Lys Lys Lys Gly Lys Glu Gln  
 115 120 125

Thr Gln Gln Pro Gln Val Lys Lys Val Asn Pro Ala Leu Lys Ala Ala  
 130 135 140

Ala Thr Ile Thr Gly Glu Gly Arg Leu Ser Ser Met Phe Thr Ser Ser  
 145 150 155 160

Ser Phe Lys Val Lys Glu Thr Asp Lys Ala Gln Tyr Glu Gly Ile  
 165 170 175

Leu Asp Glu Ile Ile Ala Gln Val Thr Pro Asp Glu Ser Asp Arg Lys  
 180 185 190

Lys His Thr Arg Arg Lys Leu Pro Gly Thr Val Pro Val Thr Ile Phe  
 195 200 205

Lys Asn Lys Lys Leu Phe Ser Val Ala Ser Ser Met Gly Met Lys Glu  
 210 215 220

Ser Glu Pro Thr Pro Ser Thr Tyr Glu Gly Asp Ser Val Ser Met Asp  
 225 230 235 240

Asn Glu Leu Met Lys Glu Glu Asp Met Lys Glu Ser Glu Val Ile Pro  
 245 250 255

Ser Glu Thr Met Glu Leu Leu Gly Ser Asp Ile Val Lys Glu Asp Gly  
 260 265 270

Ser Asn Lys Ile Arg Lys Thr Glu Val Lys Ser Glu Leu Gly Val Lys  
 275 280 285

Glu Val Phe Thr Leu Asn Ala Thr Ile Asp Met Lys Glu Lys Asp Ser  
 290 295 300

Ala Leu Ser Ala Thr Ala Gly Trp Lys Glu Ala Met Gly Lys Val Gly  
 305 310 315 320

Thr Glu Asn Gly Ala Leu Leu Gly Ser Ser Ser Glu Gly Lys Thr Glu  
 325 330 335

Phe Asp Leu Asp Ala Asp Gly Ser Leu Arg Phe Phe Ile Leu Asp Ala  
 340 345 350

Tyr Glu Glu Ala Phe Gly Ala Ser Met Gly Thr Ile Tyr Leu Phe Gly  
 355 360 365

Lys Val Lys Met Gly Asp Thr Tyr Lys Ser Cys Cys Val Val Val Lys  
 370 375 380

Asn Ile Gln Arg Cys Val Tyr Ala Ile Pro Asn Asp Ser Ile Phe Pro  
 385 390 395 400

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Ser His Glu Leu Ile Met Leu Glu Gln Glu Val Lys Asp Ser Arg Leu  
 405 410 415  
 Ser Pro Glu Ser Phe Arg Gly Lys Leu His Glu Met Ala Ser Lys Leu  
 420 425 430  
 Lys Asn Glu Ile Ala Gln Glu Leu Leu Gln Leu Asn Val Ser Asn Phe  
 435 440 445  
 Ser Met Ala Pro Val Lys Arg Asn Tyr Ala Phe Glu Arg Pro Asp Val  
 450 455 460  
 Pro Ala Gly Glu Gln Tyr Val Leu Lys Ile Asn Tyr Ser Phe Lys Asp  
 465 470 475 480  
 Arg Pro Leu Pro Glu Asp Leu Lys Gly Glu Ser Phe Ser Ala Leu Leu  
 485 490 495  
 Gly Ser His Thr Ser Ala Leu Glu His Phe Ile Leu Lys Arg Lys Ile  
 500 505 510  
 Met Gly Pro Cys Trp Leu Lys Ile Ser Ser Phe Ser Thr Cys Ser Pro  
 515 520 525  
 Ser Glu Gly Val Ser Trp Cys Lys Phe Glu Val Thr Val Gln Ser Pro  
 530 535 540  
 Lys Asp Ile Thr Ile Leu Val Ser Glu Glu Lys Val Val His Pro Pro  
 545 550 555 560  
 Ala Val Val Thr Ala Ile Asn Leu Lys Thr Ile Val Asn Glu Lys Gln  
 565 570 575  
 Asn Ile Ser Glu Ile Val Ser Ala Ser Val Leu Cys Phe His Asn Ala  
 580 585 590  
 Lys Ile Asp Val Pro Met Pro Ala Pro Glu Arg Lys Arg Ser Gly Ile  
 595 600 605  
 Leu Ser His Phe Thr Val Val Arg Asn Pro Glu Gly Thr Gly Tyr Pro  
 610 615 620  
 Ile Gly Trp Lys Glu Val Ser Asp Arg Asn Ser Lys Asn Gly Cys  
 625 630 635 640  
 Asn Val Leu Ser Ile Glu Asn Ser Glu Arg Ala Leu Leu Asn Arg Leu  
 645 650 655  
 Phe Leu Glu Leu Asn Lys Leu Asp Ser Asp Ile Leu Val Gly His Asn  
 660 665 670  
 Ile Ser Gly Phe Asp Leu Asp Val Leu Leu Gln Arg Ala Gln Ala Cys  
 675 680 685  
 Lys Val Gln Ser Ser Met Trp Ser Lys Ile Gly Arg Leu Lys Arg Ser  
 690 695 700  
 Phe Met Pro Lys Leu Lys Gly Asn Ser Asn Tyr Gly Ser Gly Ala Thr  
 705 710 715 720  
 Pro Gly Leu Met Ser Cys Ile Ala Gly Arg Leu Leu Cys Asp Thr Asp  
 725 730 735  
 Leu Cys Ser Arg Asp Leu Leu Lys Glu Val Ser Tyr Ser Leu Thr Asp  
 740 745 750  
 Leu Ser Lys Thr Gln Leu Asn Arg Asp Arg Lys Glu Ile Ala Pro Asn  
 755 760 765  
 Asp Ile Pro Lys Met Phe Gln Ser Ser Lys Thr Leu Val Glu Leu Ile  
 770 775 780  
 Glu Cys Gly Glu Thr Asp Ala Trp Leu Ser Met Glu Leu Met Phe His  
 785 790 795 800  
 Leu Ser Val Leu Pro Leu Thr Leu Gln Leu Thr Asn Ile Ser Gly Asn  
 805 810 815  
 Leu Trp Gly Lys Thr Leu Gln Gly Ala Arg Ala Gln Arg Ile Glu Tyr

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| 820   | 825  | 830  |
|---|------|------|
| Tyr Leu Leu His Thr Phe His Ser Lys Lys Phe Ile Leu Pro Asp Lys |      |      |
| 835   | 840  | 845  |
| Ile Ser Gln Arg Met Lys Glu Ile Lys Ser Ser Lys Arg Arg Met Asp |      |      |
| 850   | 855  | 860  |
| Tyr Ala Pro Glu Asp Arg Asn Val Asp Glu Leu Asp Ala Asp Leu Thr |      |      |
| 865   | 870  | 875  |
| 880   |      |      |
| Leu Glu Asn Asp Pro Ser Lys Gly Ser Lys Thr Lys Lys Gly Pro Ala |      |      |
| 885   | 890  | 895  |
| Tyr Ala Gly Gly Leu Val Leu Glu Pro Lys Arg Gly Leu Tyr Asp Lys |      |      |
| 900   | 905  | 910  |
| Tyr Val Leu Leu Leu Asp Phe Asn Ser Leu Tyr Pro Ser Ile Ile Gln |      |      |
| 915   | 920  | 925  |
| Glu Tyr Asn Ile Cys Phe Thr Thr Ile Pro Arg Ser Glu Asp Gly Val |      |      |
| 930   | 935  | 940  |
| Pro Arg Leu Pro Ser Ser Gln Thr Pro Gly Ile Leu Pro Lys Leu Met |      |      |
| 945   | 950  | 955  |
| 960   |      |      |
| Glu His Leu Val Ser Ile Arg Lys Ser Val Lys Leu Lys Met Lys Lys |      |      |
| 965   | 970  | 975  |
| Glu Thr Gly Leu Lys Tyr Trp Glu Leu Asp Ile Arg Gln Gln Ala Leu |      |      |
| 980   | 985  | 990  |
| Lys Leu Thr Ala Asn Ser Met Tyr Gly Cys Leu Gly Phe Ser Asn Ser |      |      |
| 995   | 1000 | 1005 |
| Arg Phe Tyr Ala Lys Pro Leu Ala Glu Leu Ile Thr Leu Gln Gly     |      |      |
| 1010  | 1015 | 1020 |
| Arg Asp Ile Leu Gln Arg Thr Val Asp Leu Val Gln Asn His Leu     |      |      |
| 1025  | 1030 | 1035 |
| Asn Leu Glu Val Ile Tyr Gly Asp Thr Asp Ser Ile Met Ile His     |      |      |
| 1040  | 1045 | 1050 |
| Ser Gly Leu Asp Asp Ile Glu Glu Val Lys Ala Ile Lys Ser Lys     |      |      |
| 1055  | 1060 | 1065 |
| Val Ile Gln Glu Val Asn Lys Lys Tyr Arg Cys Leu Lys Ile Asp     |      |      |
| 1070  | 1075 | 1080 |
| Cys Asp Gly Ile Tyr Lys Arg Met Leu Leu Leu Arg Lys Lys Lys     |      |      |
| 1085  | 1090 | 1095 |
| Tyr Ala Ala Val Lys Leu Gln Phe Lys Asp Gly Lys Pro Cys Glu     |      |      |
| 1100  | 1105 | 1110 |
| Asp Ile Glu Arg Lys Gly Val Asp Met Val Arg Arg Asp Trp Ser     |      |      |
| 1115  | 1120 | 1125 |
| Leu Leu Ser Lys Glu Ile Gly Asp Leu Cys Leu Ser Lys Ile Leu     |      |      |
| 1130  | 1135 | 1140 |
| Tyr Gly Gly Ser Cys Glu Asp Val Val Glu Ala Ile His Asn Glu     |      |      |
| 1145  | 1150 | 1155 |
| Leu Met Lys Ile Lys Glu Glu Met Arg Asn Gly Gln Val Ala Leu     |      |      |
| 1160  | 1165 | 1170 |
| Glu Lys Tyr Val Ile Thr Lys Thr Leu Thr Lys Pro Pro Ala Ala     |      |      |
| 1175  | 1180 | 1185 |
| Tyr Pro Asp Ser Lys Ser Gln Pro His Val Gln Val Ala Leu Arg     |      |      |
| 1190  | 1195 | 1200 |
| Met Arg Gln Arg Gly Tyr Lys Glu Gly Phe Asn Ala Lys Asp Thr     |      |      |
| 1205  | 1210 | 1215 |
| Val Pro Tyr Ile Ile Cys Tyr Glu Gln Gly Asn Ala Ser Ser Ala     |      |      |
| 1220  | 1225 | 1230 |

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Ser Ser Ala Gly Ile Ala Glu Arg Ala Arg His Pro Asp Glu Val  
 1235 1240 1245  
  
 Lys Ser Glu Gly Ser Arg Trp Leu Val Asp Ile Asp Tyr Tyr Leu  
 1250 1255 1260  
  
 Ala Gln Gln Ile His Pro Val Val Ser Arg Leu Cys Ala Glu Ile  
 1265 1270 1275  
  
 Gln Gly Thr Ser Pro Glu Arg Leu Ala Glu Cys Leu Gly Leu Asp  
 1280 1285 1290  
  
 Pro Ser Lys Tyr Arg Ser Lys Ser Asn Asp Ala Thr Ser Ser Asp  
 1295 1300 1305  
  
 Pro Ser Thr Ser Leu Leu Phe Ala Thr Ser Asp Glu Glu Ser Lys  
 1310 1315 1320  
  
 Lys Pro Ala Thr Pro Glu Thr Glu Glu Ser Asp Ser Thr Phe Trp  
 1325 1330 1335  
  
 Leu Lys Leu His Cys Pro Lys Cys Gln Gln Glu Asp Ser Thr Gly  
 1340 1345 1350  
  
 Ile Ile Ser Pro Ala Met Ile Ala Asn Gln Val Lys Arg Gln Ile  
 1355 1360 1365  
  
 Asp Gly Phe Val Ser Met Tyr Tyr Lys Gly Ile Met Val Cys Glu  
 1370 1375 1380  
  
 Asp Glu Ser Cys Lys His Thr Thr Arg Ser Pro Asn Phe Arg Leu  
 1385 1390 1395  
  
 Leu Gly Glu Arg Glu Arg Gly Thr Val Cys Pro Asn Tyr Pro Asn  
 1400 1405 1410  
  
 Cys Asn Gly Thr Leu Leu Arg Lys Tyr Thr Glu Ala Asp Leu Tyr  
 1415 1420 1425  
  
 Lys Gln Leu Ser Tyr Phe Cys His Ile Leu Asp Thr Gln Cys Ser  
 1430 1435 1440  
  
 Leu Glu Lys Met Asp Val Gly Val Arg Ile Gln Val Glu Lys Ala  
 1445 1450 1455  
  
 Met Thr Lys Ile Arg Pro Ala Val Lys Ser Ala Ala Ala Ile Thr  
 1460 1465 1470  
  
 Arg Ser Ser Arg Asp Arg Cys Ala Tyr Gly Trp Met Gln Leu Thr  
 1475 1480 1485  
  
 Asp Ile Val Ile  
 1490

<210> SEQ ID NO 33  
 <211> LENGTH: 895  
 <212> TYPE: PRT  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <223> OTHER INFORMATION: At3G59420  
  
 <400> SEQUENCE: 33

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Met | Phe | Glu | Thr | Arg | Ala | Arg | Glu | Trp | Ile | Leu | Leu | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |     |     | 15  |

Leu Val Leu Phe Thr Ser Ile Trp Gln Leu Ala Ser Ala Leu Gly Ser  
 20 25 30

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Ile | Ala | Ile | Ser | Tyr | Gly | Glu | Gly | Gly | Ser | Val | Phe | Cys |
| 35  |     |     |     |     |     | 40  |     |     |     |     |     |     |     |     | 45  |

Gly Leu Lys Ser Asp Gly Ser His Leu Val Val Cys Tyr Gly Ser Asn  
 50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Ile | Leu | Tyr | Gly | Thr | Pro | Gly | His | Leu | Gln | Phe | Ile | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |

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Thr Gly Gly Asp Gly Phe Met Cys Gly Leu Leu Met Leu Ser His Gln  
   85                   90                   95  
  
 Pro Tyr Cys Trp Gly Asn Ser Ala Phe Ile Gln Met Gly Val Pro Gln  
   100               105               110  
  
 Pro Met Thr Lys Gly Ala Glu Tyr Leu Glu Val Ser Ala Gly Asp Tyr  
   115               120               125  
  
 His Leu Cys Gly Leu Arg Lys Pro Ile Val Gly Arg Arg Lys Asn Ser  
   130               135               140  
  
 Asn Ile Ile Ser Ser Ser Leu Val Asp Cys Trp Gly Tyr Asn Met Thr  
   145               150               155               160  
  
 Arg Asn Phe Val Phe Asp Lys Gln Leu His Ser Leu Ser Ala Gly Ser  
   165               170               175  
  
 Glu Phe Asn Cys Ala Leu Ser Ser Lys Asp Lys Ser Val Phe Cys Trp  
   180               185               190  
  
 Gly Asp Glu Asn Ser Ser Gln Val Ile Ser Leu Ile Pro Lys Glu Lys  
   195               200               205  
  
 Lys Phe Gln Lys Ile Ala Ala Gly Gly Tyr His Val Cys Gly Ile Leu  
   210               215               220  
  
 Asp Gly Leu Glu Ser Arg Val Leu Cys Trp Gly Lys Ser Leu Glu Phe  
   225               230               235               240  
  
 Glu Glu Glu Val Thr Gly Thr Ser Thr Glu Glu Lys Ile Leu Asp Leu  
   245               250               255  
  
 Pro Pro Lys Glu Pro Leu Leu Ala Val Val Gly Lys Phe Tyr Ala  
   260               265               270  
  
 Cys Gly Ile Lys Arg Tyr Asp His Ser Ala Val Cys Trp Gly Phe Phe  
   275               280               285  
  
 Val Asn Arg Ser Thr Pro Ala Pro Thr Gly Ile Gly Phe Tyr Asp Leu  
   290               295               300  
  
 Ala Ala Gly Asn Tyr Phe Thr Cys Gly Val Leu Thr Gly Thr Ser Met  
   305               310               315               320  
  
 Ser Pro Val Cys Trp Gly Leu Gly Phe Pro Ala Ser Ile Pro Leu Ala  
   325               330               335  
  
 Val Ser Pro Gly Leu Cys Ile Asp Thr Pro Cys Pro Pro Gly Thr His  
   340               345               350  
  
 Glu Leu Ser Asn Gln Glu Asn Ser Pro Cys Lys Phe Thr Gly Ser His  
   355               360               365  
  
 Ile Cys Leu Pro Cys Ser Thr Ser Cys Pro Pro Gly Met Tyr Gln Lys  
   370               375               380  
  
 Ser Val Cys Thr Glu Arg Ser Asp Gln Val Cys Val Tyr Asn Cys Ser  
   385               390               395               400  
  
 Ser Cys Ser Ser His Asp Cys Ser Ser Asn Cys Ser Ser Ser Ala Thr  
   405               410               415  
  
 Ser Gly Gly Lys Glu Lys Gly Lys Phe Trp Ser Leu Gln Leu Pro Ile  
   420               425               430  
  
 Ala Thr Ala Glu Ile Gly Phe Ala Leu Phe Leu Val Ala Val Val Ser  
   435               440               445  
  
 Ile Thr Ala Ala Leu Tyr Ile Arg Tyr Arg Leu Arg Asn Cys Arg Cys  
   450               455               460  
  
 Ser Glu Asn Asp Thr Arg Ser Ser Lys Asp Ser Ala Phe Thr Lys Asp  
   465               470               475               480  
  
 Asn Gly Lys Ile Arg Pro Asp Leu Asp Glu Leu Gln Lys Arg Arg Arg  
   485               490               495

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Ala Arg Val Phe Thr Tyr Glu Glu Leu Glu Lys Ala Ala Asp Gly Phe  
 500 505 510  
  
 Lys Glu Glu Ser Ile Val Gly Lys Gly Ser Phe Ser Cys Val Tyr Lys  
 515 520 525  
  
 Gly Val Leu Arg Asp Gly Thr Thr Val Ala Val Lys Arg Ala Ile Met  
 530 535 540  
  
 Ser Ser Asp Lys Gln Lys Asn Ser Asn Glu Phe Arg Thr Glu Leu Asp  
 545 550 555 560  
  
 Leu Leu Ser Arg Leu Asn His Ala His Leu Leu Ser Leu Leu Gly Tyr  
 565 570 575  
  
 Cys Glu Glu Cys Gly Glu Arg Leu Leu Val Tyr Glu Phe Met Ala His  
 580 585 590  
  
 Gly Ser Leu His Asn His Leu His Gly Lys Asn Lys Ala Leu Lys Glu  
 595 600 605  
  
 Gln Leu Asp Trp Val Lys Arg Val Thr Ile Ala Val Gln Ala Ala Arg  
 610 615 620  
  
 Gly Ile Glu Tyr Leu His Gly Tyr Ala Cys Pro Pro Val Ile His Arg  
 625 630 635 640  
  
 Asp Ile Lys Ser Ser Asn Ile Leu Ile Asp Glu Glu His Asn Ala Arg  
 645 650 655  
  
 Val Ala Asp Phe Gly Leu Ser Leu Leu Gly Pro Val Asp Ser Gly Ser  
 660 665 670  
  
 Pro Leu Ala Glu Leu Pro Ala Gly Thr Leu Gly Tyr Leu Asp Pro Glu  
 675 680 685  
  
 Tyr Tyr Arg Leu His Tyr Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe  
 690 695 700  
  
 Gly Val Leu Leu Leu Glu Ile Leu Ser Gly Arg Lys Ala Ile Asp Met  
 705 710 715 720  
  
 His Tyr Glu Glu Gly Asn Ile Val Glu Trp Ala Val Pro Leu Ile Lys  
 725 730 735  
  
 Ala Gly Asp Ile Asn Ala Leu Leu Asp Pro Val Leu Lys His Pro Ser  
 740 745 750  
  
 Glu Ile Glu Ala Leu Lys Arg Ile Val Ser Val Ala Cys Lys Cys Val  
 755 760 765  
  
 Arg Met Arg Gly Lys Asp Arg Pro Ser Met Asp Lys Val Thr Thr Ala  
 770 775 780  
  
 Leu Glu Arg Ala Leu Ala Gln Leu Met Gly Asn Pro Ser Ser Glu Gln  
 785 790 795 800  
  
 Pro Ile Leu Pro Thr Glu Val Val Leu Gly Ser Ser Arg Met His Lys  
 805 810 815  
  
 Lys Ser Trp Arg Ile Gly Ser Lys Arg Ser Gly Ser Glu Asn Thr Glu  
 820 825 830  
  
 Phe Arg Gly Gly Ser Trp Ile Thr Phe Pro Ser Val Thr Ser Ser Gln  
 835 840 845  
  
 Arg Arg Lys Ser Ser Ala Ser Glu Gly Asp Val Ala Glu Glu Asp  
 850 855 860  
  
 Glu Gly Arg Lys Gln Gln Glu Ala Leu Arg Ser Leu Glu Glu Ile  
 865 870 875 880  
  
 Gly Pro Ala Ser Pro Gly Gln Ser Leu Phe Leu His His Asn Phe  
 885 890 895

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<210> SEQ_ID NO 34
<211> LENGTH: 451
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: At3G59430

<400> SEQUENCE: 34

Met Val Arg Lys Glu Asp Val Asp Phe Tyr Cys Gly Phe Ser Arg Lys
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Glu Leu Gln Ser Leu Cys Lys Lys Tyr Asn Leu Pro Ala Asn Arg Ser
20          25          30

Ser Ser Asp Met Ala Glu Ser Leu Ala Ser Tyr Phe Glu Lys Asn Asn
35          40          45

Leu Asn Pro Val Ser Phe Gly Val Pro Gly Asn Gln Asp Ser Ser Ala
50          55          60

Thr Thr Ser Arg Ala Pro Ala Ile Arg Thr Trp Asn Val Lys Arg Asp
65          70          75          80

Ser Tyr Gly Asn Lys Leu Asp Val Pro Arg Glu Asp Tyr Val Gln Gly
85          90          95

Ala Val Ala Arg Glu Pro Gly Ile Ile Leu Gly Asn Asn Thr Pro Tyr
100         105         110

Gln Glu Arg Asn Gly Asn Asp Gly Leu Ile Asp Phe Thr Ser Ala Pro
115         120         125

Pro Tyr Met Arg Lys Leu Asn Glu Lys Gly Pro Thr Ala Asn Ser Lys
130         135         140

Arg Ala Asp Ser Arg Leu Glu Asn Arg Met Arg Asp Val Asp Ser Gly
145         150         155         160

Asp Asn Pro Ser Ser Ser Phe Glu Phe His Val Ser Leu Glu Glu
165         170         175

Gly Ile Ser Leu Ser Val Asp Leu Asn Phe Asn Pro Ser Asp Trp Ile
180         185         190

Asn Ser Met Arg Asp Glu Val Asn Val Cys Asp Ser Met Arg Arg Arg
195         200         205

Lys Ser Pro His Ser Asp Leu Gly Ile Thr Glu Cys Lys Lys Gln Lys
210         215         220

Ser Ser Gly Gln Asp Thr Asp Gly His Val Arg Arg Glu Ser Ser Leu
225         230         235         240

Ser Pro Pro Met Lys Asp Asn Ala His Leu Pro Ser Asp His His Pro
245         250         255

Asn Gly Glu Arg Ser Leu Ala Ser Ser Ala Ile Glu Pro Cys Asn Arg
260         265         270

Ile Lys Glu Ser Ser Asp Thr Cys Lys Glu Lys Ser Gly Leu Asn Leu
275         280         285

Ser Ile Pro Asp Ser Ser Gly Pro Cys Gln Ile Ala Ser Ser Cys Val
290         295         300

Glu Ser Tyr Ser Lys Ser Cys Cys Val Asn Pro Val Asp Leu Asp Cys
305         310         315         320

Ile Ile Pro Pro Gly Lys Lys Leu Ala Ser Glu Ser Asp Met Val Ala
325         330         335

Ala Glu Gln Asn His Ser Ala Gly Asp Leu Leu Val Glu Ile Pro Lys
340         345         350

Asn Pro Ser Met Glu Ser Phe Gln Ile Val Gly Asn Ser Ser Thr Val
355         360         365

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Cys | Pro | Arg | Gly | Ala | Gly | Ser | Glu | Leu | Ser | Ser | Ser | Glu | Ala | Glu |
| 370 |     |     |     |     | 375 |     |     |     | 380 |     |     |     |     |     |     |
| Ala | Tyr | His | Ser | Asn | Gln | Pro | Cys | Ser | Pro | Arg | Lys | Thr | Ser | Arg | Ser |
| 385 |     |     |     |     |     | 390 |     |     | 395 |     |     | 400 |     |     |     |
| Ser | Thr | Ile | Ser | Ser | Pro | Glu | Phe | Ile | Ile | Asp | Arg | Glu | Ser | Thr | Ser |
|     |     |     |     |     | 405 |     |     |     | 410 |     |     | 415 |     |     |     |
| Tyr | Ser | Glu | Ser | Phe | Lys | Phe | Arg | Cys | Asn | Gly | Gly | Lys | Ser | Leu | Pro |
|     |     |     |     |     | 420 |     |     |     | 425 |     |     | 430 |     |     |     |
| Pro | Asn | Thr | Glu | Glu | Gln | Glu | Lys | Ser | Glu | Val | Leu | Ser | Glu | Gln | Ala |
|     |     |     |     |     |     | 435 |     |     |     | 440 |     |     | 445 |     |     |
| Arg | Ser | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 450 |

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The invention claimed is:

1. A method to identify a nucleic acid molecule encoding a protein involved in asymmetric cell division, comprising:
  - (1) subjecting roots of a wild type plant to a treatment inducing lateral root initiation in a synchronous way;
  - (2) subjecting roots of a mutant not developing lateral roots by a defect in auxin signalling to a treatment inducing lateral root initiation in the wild type in a synchronous way;
  - (3) identifying a nucleic acid molecule that is expressed at a higher level in the wild type plant xylem pole pericycle cells than in the mutant plant xylem pole pericycle cells using microarray analysis comprising:
    - (i) isolating xylem pole pericycle cells of the lateral root inducing portion of the wild type roots by using a xylem pole pericycle specific GFP marker line followed by cell sorting;
    - (ii) isolating xylem pole pericycle cells of the lateral root inducing portion of the mutant roots by using a xylem pole pericycle specific GFP marker line followed by cell sorting;
    - (iii) from the wild type and mutant xylem pole pericycle cells, generating nucleic acids that are used in microarray analysis and;
    - (iv) identifying a nucleic acid molecule using microarray analysis that is expressed differentially between the wild type and mutant xylem pole pericycle cells, wherein said nucleic acid molecule encodes a protein involved in asymmetric cell division comprising the sequence of SEQ ID NO: 4, or wherein said nucleic acid molecule encodes a protein involved in asymmetric cell division comprising a sequence having at least 95% sequence identity to SEQ ID NO: 4.
2. The method according to claim 1, whereby said mutant is slr-1.
3. The method of claim 1, wherein the xylem pole pericycle marker line is the GFP marker line J0121.
4. A method of modulating early lateral root initiation, the method comprising introducing into a plant or plant cell an isolated nucleic acid molecule encoding the protein of SEQ ID NO: 4 or encoding a protein having at least 95% sequence identity to SEQ ID NO: 4, wherein the nucleic acid molecule is operably linked to a heterologous promoter; and selecting a plant or plant cell for modified early lateral root initiation relative to a corresponding wild type plant or plant cell.
5. The method of claim 4, wherein the nucleic acid encodes a transcription factor.
6. A method of modulating lateral root formation comprising introducing into a plant or plant cell an expression construct for modulating asymmetric cell division comprising a nucleic acid molecule encoding a protein involved in asymmetric cell division comprising the protein of SEQ ID NO: 4 or comprising a protein having at least 95% sequence identity to SEQ ID NO: 4, wherein the nucleic acid molecule is operably linked to a heterologous promoter; and selecting a plant or plant cell for modified lateral root formation relative to a corresponding wild type plant or plant cell.
7. A method for production of a plant having modified early lateral root initiation, comprising introducing into a plant or plant cell an isolated nucleic acid molecule encoding the protein of SEQ ID NO: 4 or encoding a protein having at least 95% sequence identity to SEQ ID NO: 4, wherein the nucleic acid molecule is operably linked to a heterologous promoter; and selecting a plant for modified early lateral root initiation relative to a corresponding wild type plant.
8. The method of claim 4, wherein the nucleic acid encodes a protein comprising the sequence of SEQ ID NO: 4.
9. The method of claim 4, wherein the nucleic acid encodes a protein comprising a sequence having at least 97% sequence identity to SEQ ID NO: 4.
10. The method of claim 7, wherein the nucleic acid encodes a protein comprising the sequence of SEQ ID NO: 4.
11. The method of claim 7, wherein the nucleic acid encodes a protein comprising a sequence having at least 97% sequence identity to SEQ ID NO: 4.

\* \* \* \* \*